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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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n type F - : Clostrid : Clostrid on: S48109 h. K.D.; C. Gene probe ce number: on: S48109 prelimina se type; DN se type; DN se type; DN se type; DN	Ch 144; 144; 2TNDK: 11111 11118 111785KI 11118 11118 11118 1118 1118 1118 1118	type F - Clostrid - Jul-1995 F - Clostrid - Jul-1995 F - K 48110 F - Clostol - S 48110 F - S 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	ああああああああるコンコンコン
i Car so i	al similarity 100.0%; al similarity 100.0%; 144; Conservative 0; SYTNDKILILYFNKLYKKIKDNSII	type F - Clostr Clostridium bot Jul-1995 #seque K.D.; Collins, crobiol 31, 22 ne probes for i number: \$4810 s 48410 s 48410 1-366 <cam> treiminary; tra treiminary; tra tra tra tra tra tra tra tra tra tra</cam>	444444444 0000000000000000
sstridium botulinum botulinum squence_re re ns, M.D.; 2255-226 ridentif ridentif ridentif squinz MUID nucleic a nucleic a sequence	100 100 100 100 100 100 101 101 101 101	Clostridium bo um botulinum #sequence_revi #sequence_revi 31, 2255-262, for identific, \$48103; MUID:9, \$48103; MUID:9, \$48103; MUID:9, EMBL:X70821; Numbers of the second of th	1010 11116 1711 1711 1900 2292 2292 2292 30 56 57 73 79 97 97
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10. type F - Clostridium botulinum (fragment) s: Clostridium botulinum 12.Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999 ion: S48109 iln: K.D.; Collins, M.D.; East, A.K. Microbiol. 31, 2255-2262, 1993 Gene probes for identification of the botulinal neurotoxin gene an nce number: S48103; MUID:94013372 ion: S48109 : preliminary; nucleic acid sequence not shown; translation not sho le type: DNA s: 1-369 < CAM> s: 1-369 < CAM> s: DNA SUBDE:X70820; NID:9407790; PIDN:CAA50151.1; PID:9407791 the nucleotide sequence was submitted to the EMBL Data Library, Jan	tch 100.0%; Score 144; DB 2; Length 360; al Similarity 100.0%; Prod. No. 4e-141; 12 100.0%; Prod. No. 4e-141; 144; Conservative 0; Mismatches 0; Indels 0; Grynnorilli	ALIGNMENTS otulinum (fragment) ision 10-Nov-1995 #text. ision 10-Nov-1995 #text. ision 10-Nov-1995 #text. cation of the botulinal 94013372 n not shown NID:9407792; PIDN:CAA50:	T13167 T16112 C71625 AC71625 AC71625 C71625 C71625 C71625 C71625 C71626
_change 16-Jul-1999 neurotoxin gene and specific translation not shown 151.1; PID:9407791 L Data Library, January 1993	els 0; Gaps 0; DVYIYSTURNOF 60 TIIDCIRNUNSG 333	i 0 1	Lola-like protein hypothetical prote variant-specific s serine/threonine k genome polyprotein genome polyprotein capsid polyprotein cysteine synthase protein kinase AKI protein kinase AKI hypothetical prote tumorigenic conver hypothetical prote Rbpl protein [impo hypothetical prote knowledge hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

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C; Accession: S33411; Size C; Accession: S33411; Size C; Accession: D.E.; Hutson, R.A.; East, A.A., R; Thompson, D.E.; Hutson, R.A.; East, A.A., FEMS Microbiol. Lett. 108, 175-182, 1993
A; Title: Nucleotide sequence of the gene coding for A; Reference number: S33411; MUID:93252228
**Accession: S33411
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botulinum neurotoxin type F - Clostridium barati
C;Species: Clostridium barati
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: $33411; $31860
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C;Species: Clostridium botulinum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
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                                                                                                                                 C; Superfami.
C; Keywords:
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A; Residues: 1-1268 <THO>
A; Cross references: EMBL:X68262;
C; Superfamily: tetanus toxin
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J. Clin. Microbiol. 31, 2255-257, 1993
A;Title: Gene probes for identification of the
A;Reference number: S48103; MUID:94013372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson FEMS Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum
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A; Residues: 1-1274 < RES>
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A; Accession: I40813
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Pred. No.
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A;Molecule type: DNA, A;Residues: 1-229, 'M', 231-252 <FUJ> A;Residues: 1-229, 'M', 231-252 <FUJ> A;Cross-references: EMBL:x55180; NID:g40407; PIDN:CAA37321.1; PID:g40408 A;Experimental source: strain BL6340 C;Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter relea C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the C;Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-27,'g',29-1251 <POU>
A;Cross-references: EMBL:X62088; NID:g40379
A;Experimental source: strains ATCC 43181 and ATCC 43755
R;Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, 7
J. Gen. Microbiol. 137, 519-525, 1991
A;Title: Cloning of a DNA fragment encoding the 5'-terminus
A;Reference number: S16145; MUID:91237316
A;Accession: S16145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: JH0256; S16145
R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem. Biophys. Res. Commun. 183, 107-113, 1992
A;Title: Sequences of the botulinal neurotoxin E derived from A;Reference number: JH0256; MUID:92181428
A;Accession: JH0256
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     botulinum neurotoxin type E precursor - Clostridium butyricum C;Species: Clostridium butyricum C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change
                                                                                                                 F;2-422/Product: botulinum neurotoxin type E light chain \#status predicted <LIG>F;423-1251/Product: botulinum neurotoxin type E heavy chain \#status predicted <F;412-426/Disulfide bonds: \#status predicted
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C;Species: Clostridium botulinum
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
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C;Keywords: neurotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the
A; Reference number: S48103; MUID:94013372
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A; Residues: 1-367 <C
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      l Similarity
11; Conser
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11; Conservative
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to the EMBL Data
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A;Cross references: EMBL:X62683; NID:940397; PIDN:CANA4458.1; PID:940398
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: $48103; MUID:94013372
A;Accession: $48107
A;Reference number: $48103; MUID:94013372
A;Accession: $48107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 616-982 < CAMD
A;Resi
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A;Recession: A60027
A;Rocession: A60027
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C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111
R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P.
Eur. J. Biochem. 204, 657-667, 1992
Eur. J. Biochem. 204, 657-667, 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin A;Reference number: S21178; MUID:92174922
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A; Residues: 1-1252 <WHE>
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Local Similarity 100.0%; F
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                                                                                                                            bontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum
N;Alternate names: botulinum neurotoxin type B (BoNT/B)
C;Species: Clostridium botulinum
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A48940; S48105; S21575; A42871; S071155; S08572; S07128; S08573; S08574
R;Whelan, S. M; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.F.
Appl. Environ. Microbiol. 58, 2345-2354, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the
A;Reference number: A48940; MUID:92384550
A;Accession: A48940;
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A; Molecule type: DNA
A; Residues: 1-1291 <WHE>
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A;Molecule type: DNA
A;Mosidues: 1-1072 <STO>
A;Rosidues: 1-1072 <STO>
A;Cross-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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A;Molecule type: DNA
A;Residues: 1-1296 <FES>
A;Cross-references: EMBL:X73423; NID:g507070; PIDN:CAA51824.1; PID:g507071
C;Superfamily: tetanus toxin
                                                                                          A; Status: preliminary
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Best Local Similarity
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100.0%; Pred. No. 5.9;
ative 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatc
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A;Gene: bont/b
C;Function:
A;Gene: bont/b
C;Function:
A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevi
A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevi
C;Superfamily: tetanus toxin
C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein;
F;2-441/Product: bontoxilysin B light chain #status experimental <IGHT>
F;2-42-1291/Product: bontoxilysin B heavy chain #status experimental <HVY>
F;330,234/Binding site: zinc (His) #status predicted
F;2-31/Active site: Glu #status predicted
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A; Residues: 442-463, 'R', 465-467 <DA2>
R; Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.
Arch. Biochem. Biophys. 238, 544-548, 1985
A; Title: Partial amino acid sequences of botulinum
A; Reference number: S07128; MUID:85197963
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A;Residues: 1-313'S',315-451 <KUR>
A;Residues: 1-313'S',315-451 <KUR>
A;Experimental source: strain Okra
A;Note: sequence extracted from NCB:
R;DasGupta, B.R.; Datta, A.
Biochimie 70, 811-817, 1988
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                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 442-459 <SCH3>
R; Schiavo, G; Benfenati, F; Poulain, B; Ro
Nature 359, 832-835, 1992
A; Title: Tetanus and botulinum-B neurotoxins
A; Reference number: S27125; MUID: 93063293
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A;Molecule type: protein
A;Residues: 2-17 <SCH2>
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A:Title: Gene probes for identification of the A;Reference number: $48103; MUID:94013372
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A; Residues: 36-217, 'G', 219-224, 'S', 226-246 <SZA>
                                                                                                                                                                                                                                                                            C; Comment: Botulinum neurotoxins
                                                                                                                                                                                                                                                                                                           A; Contents:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
A; Residues: 2-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type:
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                                                                                                                                                                                                                                                                                                           annotation
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                                                                                                                                                           catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein <SCH1>
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1. 31, 2255-2262, 1993
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                                                                                                                                                                                                                                                                            inhibit neurotransmitter release
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                                                                                                                                                                                                                                                                                                                                                                                                                 Rossetto,
                                                                                                                                                                                                                                                                                                                                                           block
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                                                                                                                                                                                                                                                                                                                                                           neurotransmitter
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A; Residues: 1-1291 <RES>
A; Residues: 1-1291 <RES>
A; Cross-references: EMBL:X71343; NID:g296148; PIDN:CAA50482.1; PID:g296149
R; Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene au A; Reference number: S48103; MUID:94013372
A; Recession: S48103
A; Accession: S48103
                   C;Species: Clostridium botulinum
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T; Kurazono, H; Wille, M; Frevert, J; Wernars, K; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
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A;Molecule type: DNA
A;Residues: 634-843,'T',845,'N',847-994 <CAM2>
A;Residues: 634-843,'T',845,'N',847-994 <CAM2>
A;Cross-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781
A;Cross-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781
A;Cross-references: EMBL:X70819; NID:g40780; PIDN:CAA50150.1; PID:g407781
A;Cross-references: EMBL:X70819; NID:g40780; PIDN:CAA50150.1; PID:g407781
A;Cross-references: EMBL:X70819; NID:g40780; PIDN:CAA50150.1; PID:g407781
A;Cross-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407780; PID:g407781
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A;Residues: 634-761, 'E',763-841,'M',843,'T',845,'N',847-994 <CI
A;Cross-references: EMBL:X70814; NID:g407778; PIDN:CAA50145.1;
A;Experimental source: non-proteolytic strain 2129B (Scott)
A;Note: the nucleotide sequence was submitted to the EMBL Data
A;Accession: $48104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, Curr. Microbiol. 28, 101-110, 1994
A; Title: Nucleotide sequence of the gene coding for A; Reference number: I40631; MUID:94122659
A; Accession: I40631
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C;Date: 12-Aug-1996 #sequence_revision
C;Accession: I40631; S48103; S48104; S3
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                                                                                                                                                            N; Alternate names: botulinum neurotoxin type A
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S36015
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A:Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
C;Reywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot F;2-44/Product: bontoxilysin A light chain #status experimental <LGHT>
F;445-1296/Product: bontoxilysin A heavy chain #status experimental <HVY>
F;233,237/Binding site: Zinc (His) #status predicted
F;224/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                       R:Bloz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; J. Bloi. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495
A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
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A;Residues: 1, '0', '3-26, 'V', 28-1296 <THO>
A;Cross-references: EMBL:X52066; NII:940381; PIDN:CAA36289.1; PID:940382
A;Cross-references: MCTC 2916
A;Experimental source: MCTC 2916
R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A;Reference number: S67988; MUID:96096783
A;Accession: S68220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 2-6;445-453,'X',455-457 <DAS1>
R;DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1987
A;Title: Partial sequence of the light chain of botulinum neurotoxin type
A;Reference number: A27000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Mesidues: 867-880;1148-1217, 'Y', 1219 <GIM>
A;Experimental source: strain Hall
A;Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after ex
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A;Residues: 1-1296 <BINN
A;Cross references: GB:M30196; NID:g144864; PIDN:AAA23262.1; PID:g144865
A;Experimental source: strain 62A, subtype A
R;Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
Eur. J. Biochem. 189, 73-81, 1990
A;Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin
A;Reference number: S09492; MUID:90235864
A;Accession: S09492
                                                                                                                                                                                                                                                                                        A; Gene: atx; botA
C; Function:
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J. Protein Chem. 12, 351-363, 1993
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A; Residues: 1-12 <FUJ>
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A;Accession: A35294
A;Molecule type: DNA
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Biochimie 72, 661-664, 1990
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A; Residues: 1-35 <BET>
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A;Residues: 1-209 <KUR>
A;Cross-references: GB:AE006641; NID:gl3816031; PIDN:AAK42822.1; GSPDB:GN00155
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                   R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SSO2711 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Dete: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: G90445
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A;Experimental source: strain B31
C;Superfamily: conserved hypothetical protein MJ0240
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A;Authors: Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A: Residues: 1-209 < KUR>
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A; Residues: 1-177 < KLE>
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A;Accession: B70190
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53 NKFIDIS 59
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hypothetical protein alr4587 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: Ac2379
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sp. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2379
A;Accession: AC2379
A;Molecule type: DNA
A;Residues: 1-213 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76286.1; PID:g17133723; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
Search completed: August 15, 2002, 11:14:06 Job time: 258 sec
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C;Superfamily: biopolymer transport protein exbB-1
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Post-processing: Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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RESULT 1 \$48110 Graphics: Clostridium botulinum (f. C.Species: Clostridium botulinum (f. Species: Clostridium botulinum (f. C.Species: Clostridium botulinum (f. C.Date: 14-Jul-1995 #sequence_revision 10-No (f. C.Campbell, K.D.; Collins, M.D.; East, A.K. J. Clin. Microbiol 31, 2255-2262, 1993 J.Title: Gene probes for identification of t. A. Reference number: S48103; MUID:94013372 A. Accession: S48110 A. Status: preliminary; translation not shown A. Molecule type: DNA A. Residues: 1-366 <cam>A. Fresidues: 1-366 <cam>A. Cross-references: EMBL:X70821; NID:9407792 C. Superfamily: tetanus toxin C. Keywords: neurotoxin</cam></cam>	30 30 444 440 544 544 544 544 544 544 544 54
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um (fragment) 10-Nov-1995 #text_change 16-Jul-1999 A.K. Of the botulinal neurotoxin gene and shown 07792; PIDN:CAA50152.1; PID:g407793	307 ORF MSV146 hypothe 544 RNA polymerase sig 186 RNA polymerase sig 187 Probable GDSI-moti 195 Pyridoxal kinase (cob(I)alamin adeno ABC transporter, A type II restrictio cob(I)alamin adeno COB
\$pecific	

neurotoxin type F - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: I40813; S48108
C;Accession: I40813; S48108
R;East, A.K.; Richardson, p.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, FERS Microbiol. Lett. 96, 225-230, 1992
A,Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A,Reference number: 140644
A,Accession: I40813
A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-1274 <-RESA,Cross-references: GB:M92906; NID:g144866; PIDN:AAA23263.1; PID:g144867
R;Campbell, K.D.; Collins, M.D.; East, A.K. RESULT I40813 В δÃ В Ouery Match 35.5%; Score 153; DB 2; L Best Local Similarity 100.0%; Pred. No. 6.6e-149; Matches 153; Conservative 0; Mismatches 0; 121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMIS 153 334 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMIS 366 274 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 333 214 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 273 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60 Length 366; Indels 0; Gaps 0,

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RESULT 4

$33411

botulinum neurotoxin type F - Clostridium barati
C;Species: Clostridium barati
C;Species: Clostridium barati
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: $33411; $31860
R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Ric
R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins M.D.; Ric
                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1268 < THO>
A; Cross-references: EMBL: X68262;
C; Superfamily: tetanus toxin
C; Keywords: neurotoxin
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A;itle: Gene probes for identification of the botulinal neurotoxin gene and specific A; Reference number: S48103; MUID:94013372
A; Accession: S48108
A; Status: preliminary; translation not shown
A; Molecule type: DNA
A; Residues: 634-1002 < CAM>
A; Cross-references: EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PID:g407789
C; Keywords: neurotoxin
                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, FEMS Microbiol. Lett. 108, 175-182, 1993
A:Title: Nucleotide sequence of the gene coding for CA; Reference number: S33411; MUID:93252228
A; Accession: S33411
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C; Superfamily:
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A;Title: Gene probes for identification of the A;Reference number: S48103; MUID:94013372
A;Accession: S48109
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C;Species: Clostridium botulinum
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
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                                                                                                                                                                     Score 22; pred. No.
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Pred. No.
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Pred. No.
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9.2e-14;
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2.2e-18;
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6.7e-19;
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A; Molecule type: DNA
A; Molecule type: DNA
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A; Residues: 616-982 <CAM>
A; Rosidues: 616-982 <CAM>
A; Rosidu
                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1252 < WHE>
A; Cross-references: EMBL: X62683; NID: g40397; PI
R; Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the A; Reference number: S48103; MUID: 94013372
A; A; Accession: S48107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          botulinum neurotoxin type E precursor - Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Oct-1999 C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111 R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P. Eur. J. Biochem. 204, 657-667, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S21178; A; Accession: S21178
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The complete amino acid sequence of the Clostridium botulinum type-E neurotonce number: S21178; MUID:92174922

PIDN:CAA44558.

:1;

PID:g40398

botulinal

neurotoxin gene and

specific

acid

sequence not shown;

translation not

Library, January

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A;Molecule type: DNA, A;Molecule type: DNA, A;Molecule type: DNA, A;Residues: 1-229, W, 231-252 <FUJ> A;Residues: 1-229, W, 231-252 <FUJ> A;Cross-references: EMBL:X53180; NID:g40407; PIDN:CAA37321.1; PID:g40408 A;Experimental source: strain BL6340 C;Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter relea C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the C;Superfamily: tetanus toxin C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: EMBL:X62088; NID:g40379
A:Experimental source: strains ArCc 43181 and R:Fujii. N.; Kimura; K.; Yashiki, T.; Indoh, T J. Gen. Microbiol. 137, 519-525, 1991
A:Title: Cloning of a DNA fragment encoding th A:Reference number: S16145; MUID:91237316
A:Accession: S16145
                                                                                                                                                                                                                                    F;2-422/Product: botulinum neurotoxin type E light chain *status predicted F;423-1251/Product: botulinum neurotoxin type E heavy chain *status predict F;412-426/Disulfide bonds: *status predicted
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A;Status: nucleic acid sequence no
A;Molecule type: DNA
A;Residues: 1-27,'E',29-1251 <POU>
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A;Title: Sequences of the botulinal neurotoxin E derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum neurotoxin type E precursor - Clostridium butyricum C;Species: Clostridium butyricum C;Decies: Clostridium butyricum C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change C;Accession: JH0256; S16145
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Best Local (
                                                                                                         Matches
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983 ISDYINKWIFVTITN
                                                                                                                               Local Similarity
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                                                                                                                                  Score 15;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372
A;Accession: S48106
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C;Species: Clostridium botulinum
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
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F;1-422/Product: botulinum neurotoxin type E light chain #status predicted <LCH>
F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>
F;412-426/Disulfide bonds: #status predicted
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A;Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit ne C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the li
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A;Accession: A60027
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A;Experimental source: strain Beluga
R;Gimenez, JA.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
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R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other A;Reference number: A35294; MUID:90264400
A;Accession: B35294
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A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type A;Reference number: JH0256; MUID:92181428
A;Accession: JH0257
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A;Molecule type: DNA
A;Residues: 1-367 <CAM>
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A; Residues: 1-176, 'R
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A;Cross-references: EMBL:X62089; NID:g40393; PIDN:CAA43999.1; PID:g40394
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100.0%; Pred. No. 0.0058;
ative 0; Mismatches 0;
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 Mismatches

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A;Molecule type: protein
A;Residues: 2-47 CDAS29.
B;Reslidues: 2-47 SCDAS29.
B;Blaiz, T; Blasi, J; Yamasaki, S; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495
A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic
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A;Residues: 867-880;1148-1217,'y',1219 <GIM>
A;Residues: 867-880;1148-1217,'y',1219 <GIM>
A;Residues: 867-880;1148-1217,'y',1219 <GIM>
A;Reperimental source: strain Hall
A;Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after
R;DasGupta, B.R.; Dekleva, M.L.
Biochimie 72, 661-664, 1990
B;Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and a A;Reference number: A60025; MUID:91120847
A;Recession: A60025
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A;Molecule type: DNA
A;Residues: 1,'Q',3-26,'V',28-1296 <THO>
A;Residues: 1,'Q',3-26,'V',28-1296; NID:940381; PIDN:CAA36289.1; PID:940382
A;Cross_references: EMBL:X52066; NID:940381; PIDN:CAA36289.1; PID:940382
A;Experimental source: MCTC 2916
R;Fujita, R.; Fujinaga, Y; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin compone
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin compone
A;Reference number: S67988; MUID:96096783
A;Accession: S68220
A;Residues: 1-12 <FUJ
A;Molecular type: DNA
A;Molecular type
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A;Residues: 1-1296 <BIN>
A;Residues: 1-1296 <BIN>
A;Residues: 1-1296 <BIN>
A;Residues: 1-1296 <BIN>
A;Residues: GB:M30196; NID:gl44864; PIDN:AAA23262.1; PID:gl44865
A;Experimental source: strain 62A, subtype A
R;Thompson, D.E.; Brehn, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, Eur. J. Biochem. 189, 73-81, 1990
Bur. J. Biochem. 189, 73-81, 1990
A;Title: The complete amino acid sequence of the Clostridium botulinum type A neuroto A;Reference number: S09492; MUID:90235864
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R;Betley, M.J.; Somers, E.; DasGupta, B.R.
Biochem. Biophys. Res. Commun. 162, 1388-1395, 1989
A;Title: Characterization of botulinum type A neurotoxin gene: delineation A;Reference number: A33401; MUID:89350959
A;Accession: A33401
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A; Residues: 2-6;445-453,'X',455-457 < CDAS1>
R; DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1987
A; Title: Partial sequence of the light chain of botulinum neurotoxin type A.
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A;Molecule type: DNA
A;Residues: 1-35 <BETY
A;Cross-references: GB.M27892; NID:g144880; PIDN:AAA23269.1; PID:g551776
A;Cross-references: GB.M27892; NID:g144880; PIDN:AAA23269.1; PID:g551776
A;Coss-references: DasGupta, B.R.
J. Protein Chem. 12, 351-363, 1993
A;Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, A;Reference number: A53884; MUID:94000342
A;Accession: A53884
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97, 72, 45, 42

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C;Genetics:
A;Gene: atx; botA
C;Function:
C;Function: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptos
C;Superfamily: tetanus toxin
C;Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; tran
C;Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; tran
F;2-444/Product: bontoxilysin A light chain #status experimental <LGHT>
F;445-1296/Product: bontoxilysin A heavy chain #status experimental <HVY>
F;223,227/Binding site: zinc (His) #status predicted
F;224/Active site: Glu #status predicted
                                                                                                                                                                                                                       probable myrosinase-binding protein [imported] - Arabidopsis thaliana R; Alternate names: hypothetical protein Ti6B24.5 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001 C; Accession: T02571; G84815 F.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; R; Kounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, August 1998 A; Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence. A; Reference number: Z14679 A; Accession: T02571 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-458 <ROY. NULL STANDARD A; NULL STANDARD A; RESIDUES: TANDARD A; NULL STANDARD A; RESIDUES: TANDARD A; NOOLECULE TYPE: DNA A; Residues: 1-458 <ROY.
A;Title: Sequence a A;Reference number: A;Accession: G84815
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A;Experimental source: cultivar Columbia
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A; Title: Sequence of the gene coding for the neurotoxin of A; Reference number: I40645; MUID:94143603
A; Accession: I40645
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A; Residues: 1-1296 < RES>
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                                                                                              in, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.;
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                  Sequence and analysis of chromosome 2 of the plant Arabidopsis thalianance number: A84420; MUID:20083487
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ilarity 100.0%;
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                                                                                                                                                    Benito, M.I.; Town, C.D.; Fujii,
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Tallon, L.
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hypothetical protein CC0813 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: B87350 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: B87350 A;Status: preliminary A;Marchantary A;March
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A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: GB:AE002093; NID:g3402676; PIDN:AAC28979.1; GSPDB:GN00139
C;Genetics:
A;Gene: T16B24.5; At2g39310
                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1072 <STO>
A;Cross references: GB:AE005176; PID:g12724625;
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: A86827
Query Match
Best Local Similarity
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                                                                                                                                                                              C; Genetics:
A; Gene: yqf
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Best Local Similarity
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A; Introns: 67/3
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A;Gene: CC0813
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A; Residues: 1-540 <S
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                               0;
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                                  Mismatches
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19;
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A;Cross-references GB:M81186; NID:g144734; PIDN:AAA23211.1; PID:g144735
A;Experimental source: type B, Danish
A;Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this publical R:Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48105
A;Rocession: S48105
A;Status: preliminary
A;Status: preliminary
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C; Species: Clostridium botulinum
C; Species: Clostridium botulinum
C; Date: 19-Dec: 193 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C; Accession: A48940; 548105; 521575; A42871; S07155; S08562; S07128; S08573; S08574
C; Accession: A48940; 548105; 521575; A42871; S07155; S08562; S07128; S08573; S08574
R; Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. 56; 2345-2354, 1992
A; Title: Molecular cloning of the Clostridium botulinum structural gene encoding the type
A; Reference number: A48940
A; Accession: A48940
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A;Residues: 1-313/s/s,315-451 <KUR>
A;Residues: 1-313/s/s,315-451 <KUR>
A;Reperimental source: strain Okra
A;Rote: sequence extracted from NCBI backbone (NCBIP:109365)
R;DasGupta, B.R; Datta, A.
Biochimie 70, 811-817, 1988
A;Title: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with
A;Reference number: S07155; MUID:89000987
A;Accession: S07155
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A; Residues: 36-717, 'G', 219-224, 'S', 226-246 <SZA>
A; Residues: 36-717, 'G', 219-224, 'S', 226-246 <SZA>
A; Cross-references: EMBL: Z1193; NID: 940383; PIDN: CAA77991.1; PID: 940384
A; Cross-references: EMBL: Z1193; NID: 940383; PIDN: CAA77991.1; PID: 940384
A; Creatono, H.; Mochida, S.; Binz, T.; Eisel, U.; Quanz, M.; Grebenstein, O.; Wernars, K
J. BIO1. Chem. 267, 14721-14729, 1992
A; Title: Minimal essential domains specifying toxicity of the light chains of tetanus to A; Reference number: A42871; MUID: 92340509
A; Reference number: A42871; MUID: 92340509
A; Accession: A42871
A; Accession: A42871
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A;Molecule type: DNA
A;Residues: 634-994 <CAM>
A;Residues: 634-994 <CAM>
A;Cross-references: EMBL:X70817; NID:g407782; PIDN:CAA50148.1; PID:g407783
A;Cross-references: EMBL:X70817; NID:g407782; PIDN:CAA50148.1; PID:g407783
A;Experimental source: proteolytic type B, strain NCTC 7273
A;Experimental source: proteolytic type B, strain NCTC 7273
B;Szabo, E. A.; Pemberton, J.M.; Desmarcheller, P.M.
submitted to the EMBL Data Library, April 1992
A;Description: Partial amino acid sequence of botulinum neurotoxin type B and comparisic A;Reference number: S21575
A;Reference number: S21575
A;Reference number: S21575
                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein.
A;Molecule type: protein.
A;Residues: 442-463, 'R', '465-467 <DA2>
A;Residues: 442-463, 'R', '465-467, V.; DasGupta, B.R.
R;Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.
Arch, Biochem. Biophys. 238, 544-548, 1985
A;Title: Partial amino acid sequences of botulinum neurotoxins types B and E.
A;Reference number: S07128; MUID:85197963
A;Accession: S07128
A; Accession: S08573
A; Status: preliminary
A; Molecule type: protein
A; Residues: 2-17 <SCH2>
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A; Residues: 1-1291 <WHE>
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C;Superfamily: tetanus toxin
C;Keywords: metalloprotein; neurotoxin; transmembrane protein; zinc
F;2-441/Product: botulinum neurotoxin type B light chain #status predicted <LGHT>
F;442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HYY>
F;230,234,Pinding site: Zinc (His) #status predicted
F;231/Active site: Glu #status predicted
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A;Residues: 1-1291 <RES>
A;Cross-references: EMBL:X71343; NID:g296148; PIDN:CAA50482.1; PID:g296149
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific A;Reference number: $48103; MUID:94013372
A;Accession: $48103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2 (;Superfamily: tetanus toxin (;Superfamily: tetanus toxin (;Superfamily: tetanus toxin (;Reywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc F;2441/Product: bontoxilysin B light chain #status experimental <GHTP F;442-1291/Product: bontoxilysin B heavy chain #status experimental <GHTP F;430,234/Binding site: zinc (His) #status predicted F;231/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 442-459 <SCH3>
A;Residues: 442-459 <SCH3>
A;Residues: 442-459 <SCH3>
A;Residues: 9. Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta,
Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteo
A;Reference number: SZ7125; MUID:93063293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Folecule type: DNA A;Folecule: 634-761, E',763-841, 'M',843, 'T',845, 'N',847-994 <CAMI> A;Residues: 634-761, E',763-841, 'M',843, 'T',845, 'N',847-994 <CAMI> A;Residues: EMBL:X70814; NID:9407778; PDIN:CAA50145.1; PID:9407779 A;Cxperimental source: non-proteolytic strain 2199B (Scott) A;Experimental source: non-proteolytic 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 634-843, 'T', 845, 'N', 847-994 <CAM2>
A; Residues: 634-843, 'T', 845, 'N', 847-994 <CAM2>
A; Cross-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781
A; Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)
C; Comment: Botulinum neurotoxin type B in these strains may posses a capabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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C; Function:
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neurotoxin - Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 07-Oct.1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S39791
R;Campbell, K; Collins, M.D.; East, A.K.
Biochim. Biophys. Acta 1216, 487-491, 1993
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium A;Reference number: S39791; MUID:94092745
A;Accession: S39791
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1297 <CAM>A;Residues: 1-1297 <CAM>A;Cross-references: EMBL:X74162; NID:9441275; PIDN:CAA52275.1; PID:9441276
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
Search completed: August 15, 2002, 11:14:04 Job time: 256 sec
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S39791
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                                                                                                                    154 ISDYINKW 161
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1002 ISDYINKW 1009
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958 NNSGWKIS 965
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Title:
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Maximum DB seq length: 2000000000
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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Immunogenic type F
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AAB04085	AAG42810	AAG16790	AAG42811	AAG16791	AAR95010	AAY93310	AAY93307	AAB04081	AAY77140	AAW68390	AAR95009	AAW68391	AAY77134	~AAW68389	AAR95008	AAB04088	AAB04090	AAB04089	AAY77142	AAB04083	AAB36303	AAY77143	AAW68396	AAW68395	AAB04094	AAY77137	AAB04095	AAW68399	AAW09017	AAW09016	AAW09015	13	AAE07898
Botulism toxin C f	Arabidopsis thalia			Arabidopsis thalia	3		A manganese supero	C)	Native botulinum n	Clostridium botuli	Type A neurotoxin	Clostridium botuli	Synthetic botulinu	Clostridium botuli	eurotox	toxin	toxin	m toxin he	Ē	Botulism toxin C f	BONT/A prototoxin	Botulinum neurotox	Clostridium botuli	Clostridium botuli		Synthetic botulinu		Clostridium botuli				ic botulin	Modified clostridi

ALIGNMENTS

RESULT AAW09014	LT 1 9014
ΧĦ	AAW09014 standard; Protein; 431 AA.
AC	AAW09014;
X	
X	SI-MAK-1997 (IIISC GULIY)
XX	Immunogenic type F botulinum toxin heavy chain (aa848-1278).
Ϋ́	Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism.
S S	Clostridium botulinum type F strain Langeland.
××	
XX	WO9641881-A1.
PD	27-DEC-1996.
ı X	12-TIN-1006: 06WO-CB01400
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Y PR	12-JUN-1995, 95GB-0011909.
X PA	(MICR-) MICROBIOLOGICAL RES AUTHORITY.
X PI	Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA;
DR	WPI; 1997-065467/06.
X D	N-PSDB; AAT48100.
Tr	Immunogenic type F botulinum toxin polypeptide(s) - allows
YY Tq	recombinant vaccine prodn.
Sd	Claim 5; Page 16-17; 37pp; English.
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RESULT
AABBOOD
ID AABK
XX AAB
AC AABC
XX BOT
DT 11-J
DT 11-J
XX BOT
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Best Local Sim
Matches 431;
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                                                 Synthetic.
Clostridium
          16-NOV-2000
                              WO200067700-A2
                                                                                 infection.
                                                                                                    Botulism;
                                                                                                                       Botulism toxin heavy chain C-terminal sequence
                                                                                                                                             11-APR-2001
                                                                                                                                                                                     AAB04096 standard;
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                                                                                         recombinant
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                                                                                                                                                                                                                                                           FISKEHGWQEN 431
                                                                                                                                                                                                                                                                                        NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                        toxin; neurotoxin;
nt vector; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431
                                                 botulinum
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                                                                                                                                           (first entry)
                                                                                                                                                                                     Protein;
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                                                                                                                                                                                      432
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                                                                                         immune
                                                                                                   heavy chain; recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 431;
Pred. No. 0;
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                                                                                         response;
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                                                                                         vaccine;
                                                                                                                       (serotype
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 431; Conserv
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12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic
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                             WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
                                                                                                                                                                                                                      GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9b; 73pp; English
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99US-0133866.
99US-0133867.
99US-0133869.
99US-0133873.
99US-0146192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MP,
                                                                                                                                                                                                                                                                                                           100.0%;
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um neurotoxin
                                                                                                                                                                                                                                                                                                                                                                             botulinum serotypes A-G.
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                     Length 432;
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밁 QΥ В

Matches 431; Conservative

0,

Mismatches

0;

Indels

0; Gaps

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RESULT
AAB04103
                                                                                                                                                    Botulism neurotoxins are translated as a single 150 kDa polypeptide C chain and then posttranslationally nicked, forming a dichain C consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BONT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from clostridium botulinum serotypes A-G.
                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding the carboxy- or amino-terminal portions of
the heavy chain of botulinum neurotoxin of serotype A-G, useful as
vaccine against botulism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 18b; 73pp; English.
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12-MAY-1999;
12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botulism toxin heavy chain C-terminal sequence (serotype F).
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                                                                                                          432 AA;
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99US-0133866.
99US-0133868.
99US-0133868.
99US-0133869.
99US-0133873.
99US-0146192.
100.0%;
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Score 431;
Pred. No.
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                         DB 22;
                         Length 432;
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Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BoNT/F.
          Example 2; Page 44; 50pp; English.
                                treatment of a CNS disorder comprising a binding dometranslocates the therapeutic agent into the neuronal
                                          New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that
                                                                                 WPI; 2001-514643/56.
                                                                                                         Shone CC,
                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                          07-APR-2000; 2000GB-0008658.
                                                                                                                                                                     02-DEC-1999;
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                                                                                                                                                                                                                                                WO200158936-A2
                                                                                                                                                                                                                                                                     Chimeric - Corynebacterium diphtheriae Chimeric - Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                           Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           AAE07894;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE07894 standard; Protein; 645 AA.
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                                                                                                        Sutton JM,
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                                                                                                         Silman N;
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Best Local
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Chimeric
Chimeric
                                        superoxide
                                                       tumour;
                                                                 Neuronal cell; binding domain; translocation domain;
                                                                                                 Modified
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                                     L cell; binding domain; translocation domain; stroke; epilepsy,
infection; neurodegenerative disease; gene therapy; chimeric;
ide dismutase; SOD; botulinum neurotoxin type F; BoNT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                           clostridial heavy chain-superoxide dismutase conjugate
                                                                                                                                                                                   standard; Protein;
Bacillus stearothermophilus Influenza virus.
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Pred. No. 0;
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                                                                                                                                                          CC The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of CC all N domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC substances to neuronal cells. They are useful to treat of the CC and infection. They are also useful in gene therapy. The present sequence CC is modified clostridial heavy chain-superoxide dismutase conjugate. This CC conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa, CC chiadra for the from influenza virus and a neuronal cell-specific
                                                                                     Query Match
Best Local
                                                                       Matches 431;
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
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Chimeric -
                                                                                                                                                                                        binding domain from
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     255
                                                                                     Local Similarity
                                     ب
9
                                                                                                                                                          685 AA;
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                                                                       Conservative
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                                                                                                                                                                                        botulinum neurotoxin type F (BoNT/F).
                                                                                     100.0%;
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                                                                                     Score 431;
Pred. No. 0;
                                                                       Mismatches
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                                                                                                     Length
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The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as Hc) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC and infection. They are also useful in gene therapy. The present sequence CC is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from CC Bacillus Stearothermophilus, linker that can be cleaved by factor Xa, CC specific binding domain from botulinum neurotoxin and a neuronal cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Bacillus stearothermophilus
Chimeric - Corynebacterium diphtheriae
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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Chimeric - Corynebacterium diphtheriae.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuronal cell; binding domain; translocation domain; stroke; epileps; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                             WPI; 2001-514643/56
                                                                                            Shone CC, Sutton JM,
                                                                                                                                                           (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                          07-APR-2000; 2000GB-0008658
                                                                                                                                                                                                                                                       02-DEC-1999;
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CC Inker that can be cleaved by thrombin, translocation domain from CC diphtheria neurotoxin and a neuronal cell-specific binding domain from CC botulinum neurotoxin type F (BONT/F).
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Best Local 9
  01-NOV-2001
                             AAE07901;
                                                       AAE07901 standard;
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entry)
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Pred. No. 0;
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GIYSSKPSEVNIAQNNDIIINGRYQNESISFWVRIPKYENKVNLNNEYTIIDCIRNNNSG

giysskpsevniagnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg

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Query Match
Best Local Similarity
   Matches 431;
                                                                                                                                                                                   The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the
                                                                                                                        CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BONT/F) binding domain used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                           New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells - \frac{1}{2}
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07-APR-2000;
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tumour; infection; neur
                                                                              Sequence
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   Conservative
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2000GB-0008658
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neurodegenerative disease;
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                                       Query Match
                                                                                                                 The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                               Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; parkinson's disease; muntington's disease; motor neurone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A manganese superoxide dismutase (Mn-SOD) construct.
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 48-51; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376553/32.
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                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sutton JM,
                                                                                       1059 AA;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0024282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-GB03699.
                   100.0%; Score 431; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hallis B,
     0;
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silman N;
                                     DB 21;
 0;
   Indels
                                 Length 1059;
 0,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
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RESULT 10
AAY9317
XX
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XX
AC AAY933
AC AAY93
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Bacillus stearothermophilus.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A manganese superoxide dismutase (Mn-SOD) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1049 fiskehgwgen 1059
                                                                                                                                                            WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93312 standard; protein; 1084 AA.
                                                                                                                                                                                                                          Shone CC,
                                                                                                                                                                                                                                                                                                                                                  05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200028041-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                    (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 wkislnynkiiwtlqdtagnnqklvfnytqmisisdyinkwifvtitnnrlgnsriying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                      Sutton JM,
                                                                                                                                                                                                                                                                                                                                                  98GB-0024282
                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-GB03699
                                                                                                                                                                                                                          Hallis B, Silman N;
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Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a construct of the invention, comprising a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SOD), a Bacillus stearothermophilus Mn-SOD, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating component and the composition is cleaved to release the SOD. The composition is sufficiently sufficiently
                                                       Neuronal cell; binding domain; transl tumour; infection; neurodegenerative botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1014
                   Clostridium
                                                                                                                                            C. botulinum
                                                                                                                                                                                  01-NOV-2001
                                                                                                                                                                                                                                                              AAE07900 standard;
                                                                                                                                                                                                                                                                                                                                                                        1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ischemic stroke, trauma,
motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                               421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISKEHGWQEN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGYYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nlideksisnlgdihvsdnilfkivgcndtryvgiryfkvfdtelgkteletlysdepdp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLIDEKSISNLGDIHYSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       silkdfwgnyllynkryyllnllrtdksitqnsnflninqqrgvyqkpnifsntrlytgv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1084 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                       C2 translocation
                                                                                                                                                                                  (first entry)
                                                                          binding domain; translocation (
ion; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57-60;
                                                                                                                                                                                                                                                                  Protein; 1092 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 431;
Pred. No. 0;
                                                                                                                                     domain with BoNT/F-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                             domain; stroke; epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                              therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
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Query Match Best Local S Matches 431

Local Similarity

Conservative

100.0%; Score 431; [100.0%; Pred. No. 0; tive 0; Mismatches

DB 22; 0;

Length 1092;

0

Gaps

0,

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CC The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocates the therapeutic CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC and in of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful for delivering therapeutic CC including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum creation of the construction of the 
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent for treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2000; 2000WO-GB04644
                                                               the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Page 47; 50pp; English.
1092 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silman
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                                                                                                                                                                                  EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                          silkdfwgnyllynkryyllnllrtdksitqnsnflninqqrgvyqkpnifsntrlytgv
                                                                                                    SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                   NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
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                      NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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                                                                                                                                                                                             The invention relates to a non toxic polypeptide, for delivery of a C therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as Hc) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocates the therapeuttic agent into the neuronal cell, where the translocates the therapeuttic CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CCNS including neurodegenerative diseases, stroke, epilepsy, brain tumours CC and infection. They are also useful in gene therapy. The present sequence CC constructed by fusing the binding domain which is a hybrid of botulinum CC neurotoxin type F (BoWFF) and tetanus neurotoxin (TeNT) domain II with CC translocation domain of diphtheria neurotoxin.
                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Clostridium tetani.
Chimeric - Clostridium botulinum
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07-APR-2000; 2000GB-0008658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514643/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          botulinum neurotoxin type F; BoNT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; tetanus neurotoxin; TeNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified clostridial heavy chain fragment #5.
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12
                                                                                               Similarity
                                                                                                                                                                        660 AA;
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                                                                            Conservative
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                                                                                         49.4%; Score 213; DB 22; 100.0%; Pred. No. 5.7e-202;
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                                                                            Mismatches
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                                                                                                            Length 660;
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The invention relates to novel vaccines that induce a protective immune CC cresponse against botulinum neurotoxin (BoNT) serotypes A, B, C, D, E, F CC and G (BoNTA-BONTG). The vaccine of the invention is novel recombinant CC in the comprising a c-terminal heavy chain fragment (Hc) from BoNT CC fragment comprising a c-terminal heavy chain fragment (Hc) from BoNT CC serotypes A-G. In preferred embodiments of the invention, the vector is call venezuelan equine encephalitis virus (VEB) replicon vector. Use of this vector results in the production of large amounts of a protein encoded by a sequence cloned into the replicon. The constructs are used to produce vaccines against botulism. The proteins can also be used as collapsostic tools for the diagnosis of botulism. The transformed host collapsostic tools for the diagnosis of botulism. The transformed host collaps can be used to analyse the effectiveness of drugs and agents which collapse can be used to analyse the effectiveness of drugs and agents which collapse collapsost of the vaccine currently used against botulism is can also be used to analyse the effectiveness of drugs and agents which collapse collapsost of the vaccine formulation. The novel collapsost of the recipient. Also, the vaccine is incomplete, in that only collapsost collapso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page -; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Botulinum neurotoxin vaccine comprising a fragment from botulinum toxin serotypes A-G, is used for inducing an immune response against
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12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Botulinum neurotoxin; heavy chain; BONT; serotype F; C-terminal fragment; Venezuelan equine encephalitis virus replicon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic botulinum neurotoxin serotype F (BoNTF) C-terminal fragment.
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Matches 212
                                 Novel polypeptides (AAW09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BOMT/F). They lack the L chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g.
                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding these sequences had been optimised for codon usage for expression in yeast. Note: This sequence is not given in the specification, but is decoded from the BONTF Hc DNA sequence gi
  Sequence
                                                                                                                                                     Claim 5; Page 17-18; 37pp; English.
                                                                                                                                                                             Immunogenic type F botulinum recombinant vaccine prodn.
                                                                                                                                                                                                                                           Elmore MJ, Mauchline
                                                                                                                                                                                                                                                                    (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                              12-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum
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                         maltose binding protein
                                                                                                                                                                                                                     1997-065467/06
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  144 AA
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                                                                                                                                                                                          toxin polypeptide(s) - allows
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                                                                                                                                                                                                                                                                                                                                                                                                                                               toxin polypeptide (aa848-991).
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                         facilitate purification
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DNA sequence given
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                                                                                Novel polypeptides (AAW09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BONT/F). They lack the L chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine produ. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with maltose binding protein to facilitate purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium botulinum type F strain Langeland
                                                              Sequence
                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                           WPI; 1997-065467/06
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9641881-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botulinum toxin; neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW09016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW09016
                                                                                                                                                                                                                                     Immunogenic type {\tt F} botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                                                                                                                                                                                                                                                                          (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                    12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic type F botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 giysskpsevniagnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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                                                                                                                                                                                                               Page 18-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                              144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.4%; Score 144; DB 18; ilarity 100.0%; Pred. No. 2.7e-134; Conservative 0; Mismatches 0;
33.4%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                    Mauchline ML,
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                                                                                                                                                                                                               37pp; English.
                                                                                                                                                                                                                                                                                                     Minton
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Score 144; DB 18;
; Pred. No. 2.7e-134;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxin polypeptide (aa992-1135).
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                                                                                                                                                                                                                                                                                                     Ν̈́P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogen;
                                                                                                                                                                                                                                                                                                     Pasechnik VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                        Length
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                           Score
                                                               A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*

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9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*

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11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

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Gapop 10.0 , Gapext 0.5
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2288
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAB04096
AAB04103
AAE07893
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Immunogenic type F
Botulism toxin hea
Botulism toxin hea
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Modified clostridi
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32.5 848 22 AAB04082	32.8 472 19 AAW68394	33.1 143 18 AAW09017	33.3 144 18 AAW09016	33.6 1291 19 AAW68392	33.6 1095 21 AAY93311 A	33.6 1070 21 AAY93308	33.7 144 18 AAW09015	33.7 472 19 AAW68393	9.5 44.6 382 21 AAB36303	.5 47.2 415 22 AAB04083	8.5 47.6 847 22 AAB04081 Botulis	.5 48.1 432 21 AAY77142 Native	6.5 48.4 837 21 AAY77140 Native	1.5 48.6 435 22 AAB04090	1.5 48.6 434 22 AAB04089	3.5 48.7 462 19 AAW68390	3.5 48.7 462 17 AAR95009 T	3.5 48.7 445 19 AAW68391	3.5 48.7 438 21 AAY77134	3.5 48.7 438 19 AAW68389	3.5 48.7 438 17 AAR95008 Type	3.5 48.7 437 22 AAB04088 Bot	.5 49.0 1296 17 AAR95010 C.	.5 49.0 1092 21 AAY93310 A	0.5 49.0 1067 21 AAY93307 A	59.2 660 22 AAE07898	62.2 419 22 AAB04095	62.3 451 19 AAW68395	63.3 452 19 AAW68396	63.4 449 22 AAB04094	63.4 449 21 AAY77137 S	78.7 448 19 AAW68399 C	99.3 432 21 AAY77138
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ALIGNMENTS

XX Sq XX	PX	DR DR	ХХ	PA	XX	PF.	X PD	ΧX	S X	X X	XX	XX	XX AC	X	ID	RESULT
recombinant vaccine prodn. Claim 5; Page 16-17; 37pp; English.	Immunogenic type F botulinum toxin polypeptide(s) - allows	WPI; 1997-065467/06. N-PSDB; AAT48100.	Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA;	(MICR-) MICROBIOLOGICAL RES AUTHORITY.	12-JUN-1995; 95GB-0011909.	12-JUN-1996; 96WO-GB01409.	27-DEC-1996.	WO9641881-A1.	Clostridium botulinum type F strain Langeland.	Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism	Immunogenic type F botulinum toxin heavy chain (aa848-1278).	31-MAR-1997 (first entry)	AAWUSUL4;		AAW09014 standard: Protein: 431 AA.	RESULT 1

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RESULT
AAB04096
ID AAB0
XX AAB0
XX AAB0
XX 11-P
XX Bot.
XX Bot.
XX Fee
CX Fee
CX Synt
OS Clos
XX Synt
OS Clos
XX W02(
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Best Local Similarity
Matches 431; Conser
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                                                                                           WO200067700-A2
                                                                                                                                                   Clostridium botulinum
                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                          Botulism; toxin;
                                                                                                                                                                                                                                                                                                                                                            Botulism toxin heavy chain C-terminal sequence (serotype F).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB04096 standard;
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                                                                                                                                                                                                                                                                                                   neurotoxin;
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                                                                                                                                                                                                                                                                                                heavy chain; recombinant expression;
                                                                                                                                                                                                                                                                       immune response;
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No. 7.9e-168;
                                                                                                                                                                                                                                                                          vaccine;
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Best Local S
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12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                     expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered products also high and cost of production is lower. The nucleic acids ce be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine against botulism
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                                                                                                                               GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                             sytndkililyfnklykkikdnsildmryennkfidisgygsnisingdvyiystnrnqf
                                                                                                                                                                                                                                                                                                         SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                        silkdfwgnyllynkryyllnllrtdksitqnsnflninqqrgvyqkpnifsntrlytgv
                                                                                                        SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                       giysskpsevniaqnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg
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                                                                                                                                                                                                                                                                                                                                                             Similarity
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990S-0133866.
990S-0133867.
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990S-0133873.
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                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                             Score 2288; DB 22;
Pred. No. 8e-168;
Pred. No. 8e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATERIAL COMMAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lapenotiere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino-terminal portions of serotype A-G, useful as
                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                       Length 432;
                                                                                                                                                                                                                                                                                                                                                0;
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RESULT
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Query Match
Best Local Similarity
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12-MAY-1999;
12-MAY-1999;
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 18b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine against botulism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA54499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999;
12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant vector;
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                                                                                                                        432 AA;
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990S-0133866.
990S-0133867.
990S-0133869.
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990S-0146192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen; immune response; vaccine;
   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Middlebrook JL,
   Score 2288; DB 22; Length 432; Pred. No. 8e-168;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                           Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                  Chimeric - Corynebacterium diphtheriae Chimeric - Clostridium botulinum.
              Example 2; Page 44; 50pp; English
                                          New non toxic polypeptide for delivery of a therapeutic agent
treatment of a CNS disorder comprising a binding domain that
translocates the therapeutic agent into the neuronal cells -
                                                                                                                                                                                                     02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE07894 standard; Protein; 645 AA.
                                                                                                            WPI; 2001-514643/56.
                                                                                                                                         Shone CC,
                                                                                                                                                                                                                                                       04-DEC-2000; 2000WO-GB04644.
                                                                                                                                                                                                                                                                                       16-AUG-2001.
                                                                                                                                                                                                                                                                                                                     WO200158936-A2.
                                                                                                                                                                           (MICR-) MICROBIOLOGICAL RES AUTHORITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 fiskehgwgen 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 eviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpekiiklirtsnsn 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 silkdfwgnyllynkryyllnllrtdksitqnsnflningqrgvyqkpnifsntrlytgv 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 nlideksisnlgdihvsdnilfkivgcndtryvgiryfkvfdtelgkteietlysdepdp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 wkislnynkiiwtlqdtagnnqklvfnytqmisisdyinkwifvtitnnrlgnsriying 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 giysskpsevniaqnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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                                                                                                                                           Sutton JM, Silman N;
                                                                                                                                                                                                                         99GB-0028530.
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             stearothermophilus
                                                                                               heavy chain-superoxide dismutase conjugate
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Pred. No. 1.4e-167;
Mismatches 0;
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                             The invention relates to a non toxic polypeptide, for delivery of a C therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as He) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain (amino CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC agent into the neuronal cell, where the translocation domain is not a HN (compain of a clostridial neurotoxin and is not a fragment or derivative of CC als. The polypeptide constructs are useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC and infection. They are also useful in gene therapy. The present sequence CC is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from CC Bacillus stearothermophilus, linker that can be cleaved by factor Xa, CC specific binding domain from diphtheria neurotoxin and a neuronal cell-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells .
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Chimeric - Corynebacterium diphtheriae.
Chimeric - Clostridium botulinum.
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07-APR-2000; 2000GB-0008658.
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Chimeric - Corynebacterium diphtheriae.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
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                                   WPI; 2001-514643/56
                                                                                           Shone CC,
                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                           02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified clostridial heavy chain-superoxide dismutase conjugate #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE07892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE07892 standard; Protein; 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             852 fiskehgwgen 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     732 eviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpekiiklirtsnsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
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                                                                                           Sutton JM,
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC NS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate.

CC Mn-superoxide dismutase (MnSOD), MnSOD from Bacillus stearothermophilus, CC linker that can be cleaved by thrombin, translocation domain from CC diphtheria neurotoxin and a neuronal cell-specific binding domain from CC botulinum neurotoxin type F (BONT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 431; Conserv
 01-NOV-2001
                                                            AAE07901 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                     FISKEHGWQEN 431
                                                                                                                                                                                                NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                                                                                                                                                                                                                                                             EVIIRKNGSTDISNTDNEVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                                                                                                                                                                    nlideksisnlgdihvsdnilfkivgcndtryvgiryfkvfdtelgkteietlysdepdp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2288; DB 22; 100.0%; Pred. No. 2e-167; tive 0; Mismatches 0;
                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum CC chertoroxin translocation domain with botulinum concructs are neurotoxin type F (BONT/F) binding domain used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocates the therapeutic agent into the neuronal cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shone CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                               cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxic polypeptide for delivery of a therapeutic of a CNS disorder comprising a binding domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1032
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2288; DB 22; ilarity 100.0%; Pred. No. 2.4e-167; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
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that
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RESULT
AAY93309
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Best Local :
        Matches
                                                                                                                                The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (%n-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 48-51; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A manganese superoxide dismutase (Mn-SOD) construct.
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                                                                                                    Sequence
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          431;
100.0%; Score 2288; DB 21; Similarity 100.0%; Pred. No. 2.5e-167; 31; Conservative 0; Mismatchic.
                                                                                                    1059 AA;
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                                         DB 21; Length 1059;
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                                                                                                                                                                                                                                                                                                          Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; motor neurone disease;
                                                                                                                                                                                                                                                                                                                                                                        A manganese superoxide dismutase (Mn-SOD) construct.
                                                            WPI; 2000-376553/32.
                                                                                   Shone CC,
                                                                                                                                                                                                                                    Clostridium botulinum
                                                                                                                                                                                                                                              Homo sapiens.
Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93312 standard; protein; 1084 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1049 fiskehgwgen 1059
                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                            05-NOV-1999;
                                                                                                                                                                                      18-MAY-2000.
                                                                                                                                                                                                             WO200028041-A1
                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                               botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 FISKEHGWQEN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             809 nlideksisnlgdihvsdnilfkivgcndtryvgiryfkvfdtelgkteietlysdepdp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 wkislnynkiiwtlqdtagnnqklvfnytqmisisdyinkwifvtitnnrlgnsriying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689 giysskpsevniagnndiiyngrygnfsisfwvripkyfnkvnlnneytiidcirnnnsg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpekiiklirtsnsn
                                                                                    Sutton JM, Hallis B, Silman N;
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                     98GB-0024282
                                                                                                                                                             99WO-GB03699
                                                                                                                                                                                                                                                                                                                         trauma; Parkinson's disease;
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Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia -

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RESULT 1
AAE07900
ID AAE07900
AC AAE0
AC AAE0
XX AAE0
XX AAE0
XX Ol-N
XX Neun
KW Luma
KW Luma
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Best Local Sim:
Matches 431;
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              Clostridium
                                    Neuronal cell; binding domain; translocation domain; stroke; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                               C. botulinum
                                                                                                                         01-NOV-2001
                                                                                                                                                                                                                                                                                                         1014
                                                                                                                                                                                AAE07900 standard; Protein; 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 57-60; 65pp; English
                                                                                               C
                                                                                                                       (first entry)
                                                                                             translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2288; DB 21; 100.0%; Pred. No. 2.6e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                            domain with BoNT/F-binding domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                A
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361 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS

nslgqiivmdsignnctmnfqnnnggnigllgfhsnnlvasswyynnirkntssngcfws

eviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpekiiklirtsnsn

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BONT/F) binding domain used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non toxic polypeptide for delivery of a therapeutic agreement of a CNS disorder comprising a binding domain the translocates the therapeutic agent into the neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 47; 50pp; English.
                                                                                                   842
                                          902
                                                                                                                                                       722
                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                     Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                            1092 AA;
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2288; DB 22; 100.0%; Pred. No. 2.6e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silman
                                                                                                                                                                                                                                                                                                                                   0;
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that
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               360
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Best Local Similarity

99.3%;

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The invention relates to movel vaccines that induce a protective immune CC response against botulinum neurotoxin (BNNT) serotypes A. B. C. D. E. F. CC and G. (BNNTA-BNOTG). The vaccine of the invention is movel recombinant CC flower comprising a C-terminal heavy chain fragment (Hc) from BNNT CC serotypes A.G. In preferred embodiments of the invention, the vector is CC a Venezuelan equine encephalitis virus (VEB) replicon vector. Use of CC this vector results in the production of large amounts of a protein CC encoded by a sequence cloned into the replicon. The constructs are used CC to produce vaccines against botulism. The proteins can also be used as CC diagnostic tools for the diagnosis of botulism. The transformed host CC enlis can be used to analyse the effectiveness of drugs and agents which CC inhibit toxin effects. The vaccine currently used against botulism is CC dangerous and expensive to produce, and contains formalin, which is very CC painful for the recipient. Also, the vaccine is incomplete, in that only CC vaccine of overcomes these problems, as it is easily purified, and CC available in large quantities. It is also expressed in the lymph nodes CC synthetic BONT Hc fragments used in the present on the CC encoding these sequences had been optimised for codon usage for expression in yeast. Note: This sequence is not given in the CC specification, but is decoded from the BONTF Hc DNA sequence given on CC cancer 45-46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum neurotoxin; heavy chain; BoNT; serotype F;
C-terminal fragment; Venezuelan equine encephalitis virus replicon;
VEE; botulism; vaccine; diagnosis; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1082 fiskehgwgen 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; Page -; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Botulinum neurotoxin vaccine comprising a fragment from botulinum toxin serotypes A-G, is used for inducing an immune response against botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-1998;
12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic botulinum neurotoxin serotype F (BoNTF) C-terminal fragment.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee JS, Pushko P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
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DB; AAZ87216.
432 AA;
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99US-0133870
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Query Match

Score 2271;

DB 21;

Length 432;

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Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat humans
                                   WPI; 1998-230234/20.
N-PSDB; AAV30593.
                                                                                                             28-AUG-1996;
                                                                                                                                                                                    WO9808540-A1
                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                   Clostridium botulinum serotype F strain
                                                                                                                                                                                                                                                                                                                            Clostridium botulinum type F toxin C fragment.
                                                                                                                                                                                                                                                                                                                                                   07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 AAW68399 standard; Protein; 448 AA.
                                                                  Thalley BS, Williams JA;
                                                                                                                                       28-AUG-1997;
                                                                                                                                                              05-MAR-1998
                                                                                                                                                                                                                       Peptide
                                                                                         (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                           botulism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 fiskehgwgen 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 nslgqiivmdsignnctmnfqnnnggnigllgfhsnnlvasswyynnirkntssngcfws
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 efiirkngstdisntdnfvrkndlayinvvdrdveyrlnadisiakpekiiklirtsnsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 giysskpsevniaqnndilyngryqnfsmsfwvripkyfnkvnlnneytiidcirnnnsg
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                                                                                                                                                                                                                                                                                                                                                                                                                        13
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                                                                                                                                                                                                                                                                                                     vaccine; neurotoxin; toxin F; intoxication; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                  96US-0704159
                                                                                                                                         97WO-US15394
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                           /note= "N-terminal His tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.6e-166;
1; Mismatches 2;
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other animals at risk of intoxication with clostridial toxin

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli host cells, with the recombinant C fragment being purified on an affinity column. The invention relates to recombinant proteins derived from C. botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin contamination. Preferred hosts for production of recombinant
            C-terminal fragment; Venezuelan equine encephalitis virus replicon; VEE; botulism; vaccine; diagnosis; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins are E. coli, insect cells and yeast cells. The recombinant toxins are used as immunogens for the production vaccines and antitoxins that are useful in the treatment of P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of the histidine-tagged C fragmen of Clostridium botulinum (202F strain) type F neurotoxin, encoded by a DNA sequence (see AAVJ0593) in plasmid pETHisb. This vector can be used to express BotC soluble C fragment in Escherichia
                                          Botulinum neurotoxin; heavy chain; BoNT; serotype E;
                                                                         Synthetic
                                                                                                      08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and animals at risk
                                                                                                                                  AAY77137;
                                                                                                                                                               AAY77137 standard; Protein;
                                                                                                                                                                                                                                                                                               382
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                                                                                                                                                                                                                                                                                                          GQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWSFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLN
                                                                                                                                                                                                                                                                 KEHGWQE 430
                                                                                                                                                                                                                                                                                              gqiivmdsignnctmnfqnnngsnigllgfhsnnlvasswyynnirrntssngcfwssis
                                                                                                                                                                                                                                                                                                                                                                     IRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iliiyfnrlykkikdssildmryennkfidisgygsnisingnvylystnrnqfgiynsr
                                                                                                                                                                                                                                                                                                                                                                                                             knywgnyllynkkyylfnllrkdkyitlnsgilningqrgv-tegsvflnyklyegvevi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lsevniaqnndiiynsryqnfsisfwvripkhykpmnhnreytiincmgnnnsgwkislr
                                                                                                                                                                                                                                     kengwke
                                                                                                                                                                                                                                                                                                                                                      irkngpidisntdnfvrkndlayinvvdrgveyrlyad---tksek-ekiirtsnlndsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                       botulinum neurotoxin serotype E (BoNTE) C-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of intoxication with clostridial toxin.
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81.0%;
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                                                                                                                                                               449
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Pred. No. 2.7e-130;
3; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 448;
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Cresponse against botulinum neurotoxin (BoNT) serotypes A, B, C, D, E, F C and G (BoNTA-BONTG). The vaccine of the invention is novel recombinant CC DNA construct comprising a vector, and at least one nucleic acid C fragment comprising a C-terminal heavy chain fragment (Hc) from BONT CC serotypes A-G. In preferred embodiments of the invention, the vector is CC a Venezuelan equine encephalitis virus (VEE) replicon vector. Use of C this vector results in the production of large amounts of a protein CC encoded by a sequence cloned into the replicon. The constructs are used CC to produce vaccines against botulism. The proteins can also be used as C cells can be used to analyse the effectiveness of drugs and agents which CC inhibit toxin effects. The vaccine currently used against botulism is CC dangerous and expensive to produce, and contains formalin, which is very c paintful for the recipient. Also, the vaccine is incomplete, in that only C vaccine of overcomes these problems, as it is easily purified, and CC available in large quantities. It is also expressed in the lymph nodes CC for a better immune responses. Sequences AAY7134-Y7139 represent CC expression in vest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium botulinum Synthetic.
                               expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin
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12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serotypes
inum -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pushko P,
                                                                                                                                                                                                                                                                                                                                                                                                                          Page 43-44;
                              in yeast.
449
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99US-0133870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotoxin vaccine comprising a fragment from A-G, is used for inducing an immune response \boldsymbol{\epsilon}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith JF,
                                                                                                                                                                                                                                                                                                                                                                                                                        54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dertzbaugh MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response against
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δõ Qy 밁 Qy ₽ δÃ 밁 Qγ 망 Matches Best Local Similarity 240 146 98 61 26 sytddkilisyfnkffkriksssvlnmrykndkyvdtsgydsniningdvykyptnknqf 85 1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS 119 PSILKDFWGNYLLYNKRYYLLNLLRTDKSI-TQNSNFLNINQQRGVYQKPNIFSNTRLYT GWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYIN 179 ${\tt gwkvslnhneiiwtlqdnaginqklafnygnangisdyinkwifvtitndrlgdsklyin}$ giyndkltelnisqndyiiydnkyknfsisfwvripnydnkivnvnneytiincmrdnns 274; Conservative 63.4%; 74; Score 1451.5; DB 21; Pred. No. 1.7e-103; 4; Mismatches 70; I .. Indels Length 449; 17; Gaps 239 205

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Sequence

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RESULT 15
AAB04094
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12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
chain and then posttranslationally nicked, forming a dichain remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB04094 standard; Protein; 449 AA.
                                                                                                                                                                                                                                                                                                                                                                                               Botulism neurotoxins are translated as a single 150 kDa polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 7b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding the carboxy- or amino-terminal portions of
the heavy chain of botulinum neurotoxin of serotype A-G, useful as
vaccine against botulism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA54488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botulism; toxin; neurotoxin; heavy chain; recombinant expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botulism toxin heavy chain C-terminal sequence (serotype E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant vector; antigen; immune response; vaccine; bacterium;
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99US-0133869.
99US-0133873.
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99US-0133866.
99US-0133867.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
434 gcfwnfiseehgwge 448
                                                                                                                                                                                                                                                                                                                                        180 GNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPD 239
                                                                                                                                                                                                                                                                                                                                                                                                                               120 GWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYIN 179
                                                                             375 -sssgnrfngvvvmnsvgnnctmnfknnngnnigllgfkadtvvastwyythmrdhtnsn 433
                                                                                                                  356 TSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSN 415
                                                                                                                                                        321 gikvkiqrvnnsstn----dnlvrkndqvyinfvaskthlfplyadtattnkektiki--
                                                                                                                                                                                                                                   266 tnilkdfwgnyllydkeyyllnvlkpnnfidrrkdstlsinnirs----tillanrlys
                                                                                                                                                                                                                                                                                                                   206 gnlidqksilnlgnihvsdnilfkivncsytryigiryfnifdkeldeteiqtlysnepn
                                                                                                                                                                                                                                                                                                                                                                                                146 gwkvslnhneiiwtlqdnaginqklafnygnangisdyinkwifvtitndrlgdsklyin
                                     416 GCFWSFISKEHGWQE 430
                                                                                                                                                                                                299 GVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKIIKLIR 355
                                                                                                                                                                                                                                                                           240 PSILKDFWGNYLLYNKRYYLLNLLRTDKSI-TQNSNFLNINQQRGVYQKPNIFSNTRLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 giyndkltelnisqndyiiydnkyknfsisfwvripnydnkivnvnneytiincmrdnns 145
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63.0%; Pred. No. 1.7e-103;
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Search completed: August 8, 2002, 09:42:45 Job time: 219 sec

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Result
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Copyright (c) 1993 - 2000 Comp
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Best Local
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EMBL; X70816; CAA
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MEROPS; M27.002;
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                                                                  "Sequences of the botulinal neurotoxin E derived botulinum type E (strain Beluga) and Clostridium ATCC 43181 and ATCC 43755)."
                                                                                                                                                                STRAIN=BELUGA;
MEDLINE=92181428; PubMed=1543481;
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
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  SEQUENCE FROM N.A
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MISCELLANEOUS: THERE ARE SEVEN AUTIGENICALLY
BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, F
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) ANI
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIV
WHILE THE N-AND C-TERWINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
FORMATION AND TOXIN BINDING, RESPECTIVELY.
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27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00760; BONTOXILYSIN.
                                           Biophys.
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Transmembrane; Hydrolase; Metalloprotease; Zinc.
1 436
BOTULINUM NEUROTOXIN F, LIGHT-CHA
437 1274
BOTULINUM NEUROTOXIN F, HEAVY-CHA
227 227
ZINC (CATALYTIC) (BY SIMILARITY).
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231 ZINC (CATALYTIC) (BY SIMILARITY)
429 445
INTERCHAIN (PROBABLE).
1274 AA; 146709 MW; 5B99756A7438B921 CRC64;
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larity 100.0%;
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AAC60475.1;
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. 26, Last sequence update)
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toxin type E precursor (EC 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90344918; PubMed-211 Gimenez J.A., Dasgupta B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85197963; PubMed-3888113;
Schmidt J.J., Sathyamoorthy V., Dasgupta B.
"Partial amino acid sequences of botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92174922; PubMed-1541280; Whelan S.M., Elmore M.J., Bodsworth N.J., Atkinson T., Minton N.P.; Whelan S.M., Elmore M.J., Bodsworth N.J., Atkinson T., Minton N.P.; "The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
             EMBL; X62089; CAA43999.1; EMBL; X62683; CAA44558.1;
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                              +
                                                                                                                                                                                                                                                                                                                                                                                       "Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
J. Biol. Chem. 269:1617-1620(1994).

-i- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNAL AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS INHIBITIS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERILASE THAT CATALYZES THE HYDROLYSIS OF THE 180-ARG-|-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94124495;
Binz T., Blasi J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schiavo G., Santtuci A., Dasgupta B.R., Benfenati F., Wilson M.C., Montecucco C
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                                                                                                                                                                                                                        neuroexocytosis apparatus, synaptobravins, SNAP25 or syntax detected action on small molecule substrates. SUBUNIT: DISULFIDE-LINED HETERODIMER OF A LIGHT CHAIN (L) HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL AC WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANN FORMATION AND TOXIN BINDING, RESPECTIVELY.

SUBCELLULAR LOCATION: Secreted.

NISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS
                                                                                                                                                                                            BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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T., Kurazono H., Wille M., Frevert J.,
complete sequence of botulinum neuroto:
other clostridial neurotoxins.";
iol. Chem. 265:9153-9158(1990).
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                                                              requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                            non-profit institutions as long and this statement is not removed.
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, Yamasaki S., B
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Best Local
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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AND ATCC 43755;

STRAIN-ATCC 43181, AND ATCC 43755;

MEDLINE-92181428; PubMed-1543481;

POULET S., Hauser D., Quanz M., Niemann H., Popoff M.R.;

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                                                              MEDLINE=91237316; PubMed=203376; Fujil N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; Yokosawa N., Yashiki T., Oguma K.; "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Bontoxilysin E).
Clostridium butyricum.
Bactlius/Clostridium group; Clostridiaceae;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
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PRINTS; PR00760; BONTOXIIXSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1
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InterPro; IPR000130;
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       SEQUENCE OF 1-48
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R > G (IN REF. 2).

C -> S (IN REF. 2 AND 3).

R -> A (IN REF. 2).

I -> L (IN REF. 2).

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STANL...

P10845; P18639; P01561;

01-JUL-1989 (Rel. 11, Created)

01-JUL-1993 (Rel. 26, Last sequence update)

01-JUL-1993 (Rel. 26, Last sennotation update)

101-MAR-2002 (Rel. 41, Last annotation update)

Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)

"Torrinxilysin A) (BOTOX) (Contains: Botulinum neurotoxin A, 1
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INIT_MET
CHAIN
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ENDOPEPTIDASE

I- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.

I- SUBUNIT: DISULFIDE-LIMED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, HEAVY CHAIN OCTIVITY, OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

I- SUBCELLULAR LOCATION: Secreted.

I- MISCRLAUROUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

I- SIMILARITY: BELONGS TO DEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gimenez J., Foley J., Dasgupta B.R.;

"Neurotoxin type E from Clostridium botulinum and C. butyricum;

partial sequence and comparison.";

FASSEB J. 2:A1750-A1750(1998).

-i- FUNCTION: BOYULTUNUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as Its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JH0256; JH0256.
PIR; S16145; S16145.
HSSP; P10845; 3BTA.
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Gimenez J.,
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ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1
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                                                                                                                                                                                                                                                         982 ISDYINKWIFVTITN 996
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                                                                                                                                                                                                                                                                                                                                1 Similarity
15; Conserv
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Botulinum

neurotoxin

A, heavy-chain].

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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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"Partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.; "Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component."; Int. J. Syst. Bacteriol. 46:1105-1112(1996).
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    Sathymoorthy
                           MEDLINE-89024662;
                                              SEQUENCE OF 448-464 AND 872-895
                                                                                      "Botulinum neurotoxin type A: sequence N-terminus and around the nicking site sichimie 72:661-664(1990).
                                                                                                                                                           Dasgupta
                                                                                                                                                                                   MEDLINE=91120847;
                                                                                                                                                                                                                                                    "Partial sequence
Biochemistry 26:41
                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89350959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96096783;
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                                                                                                                                                                                                                                               OF 1-46.

B.R., Foley J., Niece R sequence of the light c. stry 26:4162-4162(1987).
                                                                                                                                                           B.R., Dekleva M.L.
                                                                                                                                                                                                     OF 1-5 AND 444-456
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Biophys. Res. Commun.
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PubMed=3178218;
Dasgupta B.R., F
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chain
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    Foley
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o forms of nontoxic-nonhemagglutinin
um type A progenitor toxins.";
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heavy and
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oxin type
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Jahn
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MEDLINE=98455071; PubMed=9783750;
Lacy D.B., Tepp W., Cohen A.C., D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Site-directed mutagenesis identifie
"Site-directed mutagenesis identifie
light chain of botulinum neurotoxin
Biochem. Biophys. Res. Commun. 288:]
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Shone C.C., Hambleton P., Melling J.;
"Inactivation of Clostridium botulinum type
and purification of two tryptic fragments. F
the COOH-terminus of the heavy subunit destr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for toxicity.";
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Benfenati F., Wilson M.C., Montecucco
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                                                                                                                                        PHARMACEUTICAL: Available under the name BOTOX(R) (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction. MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-1-Arg-198 bond in SNAP-25, thereby blockin neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Limited hydrolysis of proteins
                                                                                                                                                                                                                                                                                                                                                  heavy chain (H).
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                             neuroexocytosis apparatus, synaptobravins, SNAP2: detected action on small molecule substrates. SUBUNIT: Disulfide-linked heterodimer of a light
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Niemann H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. 151:75-82(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f SNAP-25 by types E and 269:1617-1620(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBSTRATE.
PubMed=8243676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBSTRATE. PubMed=8294407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5:898-902(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of botulinum neurotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHE-265 AND
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266:142-151(1988).
                                                                                                                                                                                                                                                                                                                                                     Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    son E.A., Montecucco C., Rossetto O.; identifies active-site residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coxin type a.";
288:1231-1237(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragments. Prote
subunit destroys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dasgupta
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R.,
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                                                                           EMBL
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                                                                              a collaboration - MBL outstation
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EMBL; M30196; AAA23262.1; -.
EMBL; X92973; CAA63551.1; -.
EMBL; D67030; BAA11051.1; -.
EMBL; M77892; AAA23269.1; -.
PIR; A35294; BTCLAB.
PIR; S09492; S09492.
PDB; 3BTA; 01-0CT-99.
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                  045894; P77780;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Re
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ACT_SITE
STRAIN-Kyoto-F;

MEDLINE-9414503; PubMed-8310180;

Willems A., East A.K., Lawson P.A., Collins M.D.;

"Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison wi
                                                                                                                                                                                    BOTA OR BNA OR ATX.
Clostridium botulinum.
Bacteria; Firmicutes;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
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                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=1491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000130; zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; M27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 WIFVTITNNRL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000395; Bontoxilysin.
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑĄ.
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1295
222
223
226
261
261
1279
646
675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 11; DB 1; 100.0%; Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149322
                                                                                                                                                                                                   Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY.

F->A: DECREASE IN ENZYMATIC ACTIVITY.

Y->A: DECREASE IN ENZYMATIC ACTIVITY.

Y->A: DECREASE IN ENZYMATIC ACTIVITY.

P-> Q (IN REF. 1).

E-> P (IN REF. 9).

F-> L (IN REF. 8).

S-> K (IN REF. 8).

22 MW; 858342F754862579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
V -> A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOTULINUM NEUROTOXIN A, BOTULINUM NEUROTOXIN A, ZINC (CATALYTIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1295 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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            with
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gene encoding the nontoxic nonhemagglutinin component.;

Int. J. Syst. Bacteriol. 46:1105-1112(1996).

C. I- FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesticle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gh-1-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure (By similarity).

C. TATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.

C. BUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity).

SUBCELLAUROUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl. D, E, F, and G.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                     Matches
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TRANSMEM
SEQUENCE
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ACT_SITE
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1013 WIFVTITNNRL 1023
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ProDom; PD001963;
PROSITE; PS00142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X73423; CAA51824.1; -. EMBL; X87974; CAA61234.1; -. HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97016817; PubMed=8863443; East A.K., Bhandari M., Stacey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other clostridial neurotoxins."; Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000395; Bontoxilysin.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; M27.002
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                                                                        161 WIFVTITNNRL 171
                                                                                                                                                                                             Similarity
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                   AA;
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ZINC_PROTEASE; FALSE_NEG.
membrane; Hydrolase; Metalloprotease; Zinc.
0 BY SIMILARITY.
                                                                                                                                                                                         2.6%;
                                                                                                                                                                                                                                                                                                                                                       149279
                                                                                                                                                                                                                                                                                                                                                                                                                      BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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                                                                                                                                                                                             Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                   5DA04A13D98D6372 CRC64;
                                                                                                                                                                                         DB 1;
0.0065;
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RESULT 7

BXB_CLOD
ID BXB_C
ID BXB_C
ID 01-JU
DT 01-JU
DT 01-MA
DE BOTH
GN BOTH
GN BOTH
GN Clost
OC Clost
OC CLOST
RN (11)
RP SEQUE
RX MEDLI
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                                                                                         BXE_CLOBO
BXE_CLOBO

1 P10844; P10843;
1 01-JUL-1989 (Rel. 11, Created)
1 01-JUL-1993 (Rel. 26, Last sequence updat
1 01-MAR-2002 (Rel. 41, Last annotation up
1 01-MAR-2002 (Rel. 41, Last annotation up
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
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080950;
16-OCT-2001
16-OCT-2001
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16-OCT-2001 (Rel. 40, Last annotation update)
Myrosinase binding protein-like At2g39310.
AT2G39310 OR T16B24.5.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Goodman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
SEQUENCE FROM N.A. MEDLINE=92384550;
                                         Clostridium.
NCBI_TaxID=1491;
                                                                    Clostridium botulinum Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001229; Jacal Pfam; PF01419; Jacalin; 3. Lectin; Repeat; Multigene SEQUENCE 458 AA; 50463
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC004697;
HSSP; P18674; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20083487; PubMed=10617197;
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 PubMed=1514783;
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J. Biol.
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J. Clin.
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Szabo E.A., Pembertor
Submitted (APR-1992)
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                                             This
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                                                                                                                                                                                                                                                                                                              Schiavo G., Benfenati F., Poulain Dasgupta B.R., Montecucco C.;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93054694; PubMed-1429690; Schlavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco "Botulinum neurotoxins are zinc proteins."; J. Biol. Chem. 267:23479-23483(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Botulinum neurotoxin type B (strain 657):
similarity with tetanus toxin.";
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        the European Bioinformatics Institute. The hy non-profit institutions as long
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MEDLINE=93063293; PubMed=1331807;
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                                                                                                              CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or Syntaxin. No detected action on small molecule substrates.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILLE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                               SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT
BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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probes for identification of the botulinal reprobes for identification of neurotoxin types B, E,
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Pemberton
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EMBL/GenBank/DDBJ
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EMBL; Z11934; CAA77991.1; -.
EMBL; Z01934; CAA50148.1; -.
PIR; S07128; S07128.
PIR; S07128; S07128.
PIR; S07155; S07155.
PIR; S08562; S08562.
PIR; S08573; S08573.
PIR; S08573; S08573.
PIR; S08574.
PIR; A48940; A48940.
HSSP; P10845; 3BTA.
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         STRAIN-113 / 30;

MEDLINE-94092745; PubMed-8268233;

Campbell K., Collins M.D., East A.K.;

Campbell K., Collins M.D., East A.K.;

"Nucleotide sequence of the gene coding for Clostridium botulinum

(Clostridium argentinense) type G neurotoxin: genealogical comparison

with other clostridial neurotoxins: ";

Biochim. Biophys. Acta 1216:487-491(1993).

BIOCHIM. BIOCHIMUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY METROGRADE TRANSPORT UP THE XXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEL POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
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CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                    BXG_CLOBO STANDARD; PRT; 1296 AA. 60393; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BONT/G)
                                                                                                                                                                                                                                                               Clostridium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
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ACT_SITE
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=1491;
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INIT_MET
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
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ENDOPEPTIDASE.
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8; Conserv
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229 2
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1290 AA;
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BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
1290
BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
229
ZINC (CATALYTIC) (BY SIMILARITY).
230
BY SIMILARITY).
233
ZINC (CATALYTIC) (BY SIMILARITY).
11TERCHAIN (PROBABLE).
29
T -> M (IN REF. 4).
217
R -> G (IN REF. 2).
217
R -> S (IN REF. 2).
3463
S -> R (IN REF. 4).
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S -> R (IN REF. 4).
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Best Local
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SEQUENCE
        SEQUENCE FROM N.A.
STRAIN-DSM 1728;
MEDLINE-20479972; PubMed=11029001;
MEDLINE-20479972; PubMed=11029001;
MEDLINE-20479972; PubMed=11029001;
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.",
Nature 407:508-513(2000).

NATURE 407:508-513(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.
-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TEXHINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.
-!- SUBCELULAR LOCATION: Secreted (By similarity).
-!- MISCELLAREOUS: THERE ARE SEVEN ANTIGENERCALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.
                                                                                                                                                                                                Thermoplasma acidophilum.
Archaea; Euryarchaeota; T
                                                                                                                                                                                                                                                             09HLI3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                     NCBI_TaxID=2303;
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InterPro; IPR000130; Zn_MTpeptdse
Pfam; PF01742; Peptidase_M27; 1.
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INIT_MET 0 (
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229 2
230 2
233 2
435 AA;
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BY SIMILARITY
                                                                                                                                                                                                 Thermoplasmales; Thermoplasmaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8; DB;; Pred. No. 8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOTULINUM NEUROTOXIN G, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN G, HEAVY-CHAIN.
ZINC (CAFALYTIC) (BY SIMILARITY).
BY SIMILARITY:
ZINC (CAFALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
MW; DC8E47E15F665C31 CRC64;
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                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                259
                                                                                                              Transferase; Co
SEQUENCE 267
                                                                                                                                                     EMBL; AE000332; AAC75512.1; -.
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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Pfam; PF00578; AhpC-TSA; 1.
Antioxidant; Complete proteome.
ACT_SITE 40 40 BY
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                                                                                                                                                                                                                                                                                                                 FUNCTION: CONVERTS CNB12 TO ADOB12 CATALYTIC ACTIVITY: ATP + cob(I)ale
                                                                                                                                                                                                                                                                                             PATHWAY: ETHANOLAMINE UTILIZATION.
                                                                                                                                                                                                                                                                                                           diphosphate + adenosylcobalamin
              LLNLLRT
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Similarity
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ase; Complete proteome.
ase; AA; 30171 MW;
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                                                     Score 7; pred. No
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Best Local
  01-APR-1990
01-APR-1990
01-JUN-1994
AL1 protein
                                                                                          VAL1_CLVK
P14982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McClelland M., Sanderson K.E., Spieth J., Cli
Courtney L., Porwollik S., Ali J., Dante M.,
Leonard S., Nguyen C., Scott K., Holmes A., C
Ryan E., Sun H., Florea L., Miller W., Stonek
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTT_SALTY
Q9ZFV4;
30-MAY-2000
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SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CONVERTS CNB12 TO ADOB12 (BY -!- CATALYTIC ACTIVITY: ATP + cob(I)alamin diphosphate + adenosylcobalamin. -!- PATHWAY: ETHANOLAMINE UTILIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-IT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kofoid E.C., Rappleye C.A., Stojiljkovic I., Roth J.R.; "The 17-gene ethanolamine (eut) operon of Salmonella typhimurium encodes five homologues of carboxysome shell proteins."; J. Bacteriol. 181:5317-5329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99395039; PubMed=10464203;
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267 AA; 30238 MW;
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M., Du F., Hou S
A., Grewal N., M
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+ H(2)0 = phosphate
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N., Mulvaney E.
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Best Local :
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P14972;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90174930; PubMed=2308831; Morris B., Coates L., Lowe S., Richardson K., Eddy P.; Nucleotide sequence of the infectious cloned DNA components African cassava mosaic virus (Nigerian strain)."; Nucleic Acids Res. 18:197-198(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cassava latent virus (strain Nigerian).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus
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InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATAL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 301:260-262(1983).
-I- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cassava latent virus (strain West Kenyan 844).
Viruses; ssDNA viruses; Geminiviridae; Begomov
                                                                                                                            EMBL; X17095; CAA34953.1; -. PIR; S07594; S07594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids res. 18:197-198(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding.
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PIR: S07594; S07594.
InterPro; IPRO01191; Gemini_ALl.
Pfam; PF00799; Gemini_ALl; 1.
PRINTS; PR00227; GEMCOATAL1.
ProDom; PD000736; Gemini_ALl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10819;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 TITNNRL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 TITNNRL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
mes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD000736; Gemini_AL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 7; DB 100.0%; Pred. No. 27 Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
; ED173E753EE92D69 CRC64;
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io. 27;
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RESULT
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Best Local Similarity
Thes 7; Conserv
Query Match
Best Local S
Matches 7
                                                                                                           EMBL; L19443; AAC13979.1; -.
EMBL; M28822; AAA02333.1; -.
PIR; A40048; ERADI4.
InterPro; IPR000939; Adeno_fiber2.
InterPro; IPR000978; Adeno_fibre.
InterPro; IPR000931; Adeno_fibre.
Pfam; PF00541; adeno_fiber; 1.
Pfam; PF00608; adeno_fiber2; 5.
                                                                                                                                                                                                                                                                                                            P18048;
01-NOV-1990 (Rel. 16, Created)
01-FEB-1996 (Rel. 33, Last sequ
01-FEB-1996 (Rel. 33, Last anno
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93297140; PubMed=8517033; MEDLINE=93297140; PubMed=8517033; MEDLINE=93297140; PubMed=8517033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-94087748; PubMed-8263936; Davison A.J., Telford E.A., Watson M.S., McBride K., Mautner V.; "The DNA sequence of adenovirus type 40."; J. Mol. Biol. 234:1308-1316(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fiber protein 2.
Human adenovirus type 40
                                                                         Fiber protein CONFLICT 2
                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 167-387 FROM N.A MEDLINE=89370295; Pubmed=277
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kidd A.H., Chroboczek J., Cusack S., "Adenovirus type 40 virions contain Virology 192:73-84(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=28284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIB2_ADE40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TITNNRL 74
 Local Similarity 100.0%; nes 7; Conservative 0;
                                                                                              PR00307; ADENOVSFIBRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dsDNA viruses,
                                                              226
387 #
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                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=2773314;
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40435 MW;
                                                              226
41346 MW;
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100.0%; Pred. N
           1.6%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no RNA stage; Adenoviridae; Mastadenovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                              G -> S (IN REF. 2 AND 3).; 11A3C1FCD61A3ACB CRC64;
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            two distinct fibers.";
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o. 27;
                         DB 1;
                                                                                                                                                                                                                                                                                                                                                           SERVES AS THE LIGAND
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                         Length 387;
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RESULT 15
FIR2_ADE41
ID FIR2_A
Search completed: August 15, 2002, 11:24:37 Job time: 684 sec
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X17016; CAA34882.1; -.
EMBL; M60327; AAA42505.1; -.
PIR; S09217; ERADN1.
PIR; A45352; A45352.
HSSP; P11818; IKNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1990
01-NOV-1995
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Human adenovirus type 41.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10524;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000939; Adeno_fiber2.
InterPro; IPR000978; Adeno_fiber_knob.
InterPro; IPR000931; Adeno_fibre.
Pfam; PF00541; Adeno_fiber; 1.
Pfam; PF00608; Adeno_fiber2; 5.
PFINTS; PR00307; ADENOVSFIBRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kidd A.H., Erasmus M.J., Tiemessen C.T.;
"Fiber sequence heterogeneity in subgroup F adenoviruses.";
Virology 179:139-150(1990).
-!- FUNCTION: RECOGNIZES THE CELL RECEPTOR; SERVES AS THE LIGAND BETWEEN THE ADENOVIRUS CAPSID AND THE HOST CELL RECEPTOR.
-!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human enteric adenovirus type 41 (Tak) contains a second fiber protein gene.";
Nucleic Acids Res. 18:1901-1901(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91021015; PubMed=2219717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 337-387 FROM N.A. STRAIN-FB585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90245595; PubMed=2336370; Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                        358 NSNNSLG 364
                                                                                                                                       9
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                                                                                                                                       NSNNSLG
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                                                                                                                                                                                                                                                 Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            AA;
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15,
32,
                                                                                                                                                                                                                                                                                                                                                                                         41397 MW; 8652E785276573C7 CRC64;
                                                                                                                                                                                                                                            1.6%; Score 7; DB 100.0%; Pred. No. 29 cive 0; Mismatches
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Velarde J. Jr.,
                                                                                                                                                                                                                                                                                                  Length 387;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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Perfect score:
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1: | SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: | SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

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4: | SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*

5: | SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*

6: | SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*

7: | SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*

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Immunogenic type F
Immunogenic type F
Botulism toxin hea
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Modified clostridi
C. botulinum C2 tr
A manganese supero
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Result No.

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m 5; Page 17-18; 37pp; Englis l polypeptides (AAW09014-17)	Immunogenic type F botulinum toxin recombinant vaccine prodn.	; 1997-065467/06.	re MJ, Mauchline ML, M	R-) MICROBIOLOGI		- TEN - 1896 : 0650 -	641881-	lostridium botulinum type F strain	Botulinum toxin; neurotoxin; BoBT,	Immunogenic type F botulinum toxin	1-MAR-1997 (first entry)	AAW09015;	T 1 015 AAM09015 standard; Protein; 144 AA	AL	144 100.0 1084 21 AAY993112 144 100.0 1092 22 AAE07900 88 61.1 43 21 AAY97313 26 18.1 448 21 AAW68395 11 7.6 449 21 AAW68395 11 7.6 449 21 AAW68395 11 7.6 449 21 AAW68395 11 7.6 445 11 AAW68395 11 7.6 445 12 AAB04089 8 5.6 432 21 AAY77142 8 5.6 433 21 AAY77142 8 5.6 435 22 AAB04089 8 5.6 437 22 AAB04089 8 5.6 438 17 AAR95008 8 5.6 438 19 AAW68398 8 5.6 439 22 AAB04089 8 5.6 439 21 AAY77134 8 5.6 440 22 AAB04089 8 5.6 440 22 AAB04089 8 5.6 440 22 AAB04089 8 5.6 440 21 AAW68391 8 5.6 472 19 AAW68391 8 5.6 472 19 AAW68394	
h. respectively comprise	<pre>polypeptide(s) -</pre>		NP, Pasechnik VA;	RITY.				in Langeland.	/F; immunogen; vaccine;	polypeptide (aa848-			Α.	ALIGNMENTS		
amino acids	allows								e; botulism.	991).					A manganese supero C. botulinum C2 tr Synthetic botulinum C2 tr Synthetic botulinu C2 tr Synthetic botulinu clostridium botuli Botulism toxin hea Synthetic botulinu Botulism toxin beat Clostridium botuli Botulism toxin clostridium toxin cas Botulism toxin hea Botulism toxin heat botulism toxin botulinu Botulism toxin heat Clostridium botuli Type A neurotoxin clostridium botuli Amanganese supero A manganese supero	

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Best Local
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848-1278) of a type F botulinum neurotoxin (BONT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but induce protective immunity to a type F botulinum toxin, making t useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g
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                                                                                                                A polypeptide
848-1278) of a
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                                                                                                                                                            Claim
                                                                                                                                                                                     Immunogenic type F botulinum toxin recombinant vaccine prodn.
                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxin;
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Pred. No. 2.8e-141;
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                             making them
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12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
29-JUL-1999;
Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BONT) can be used in recombinant expression vectors and expressed in transformed cells to produce
                                                                               Claim
                                                                                                             the
                                                                                                                     New
                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                           12-MAY-2000;
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DB; AAA54490.
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                                                                                                                                                                                                                                                                                                                                                                                                       toxin;
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99US-0133869.
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                                                                                                                                                                                          MEDICAL
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or; antigen;
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Pred. No. 7.6e-141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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RESULT
AABO4103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 144
                                                                                                                                                                                                                                             12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from clostridium botulinum serotypes A-G.
Disclosure; Fig 18b; 73pp; English.
                                                                                             N-PSDB;
                                                                                                                                       Smith LA,
                                                                                                                                                                                                                                                                                                                       12-MAY-2000; 2000WO-US12890
                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                     WO200067700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB04103 standard; Protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                New nucleic acids encoding the carboxy- or amino-terminal portions of
the heavy chain of botulinum neurotoxin of serotype A-G, useful as
vaccine against botulism
                                                                                                                                                                    (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                    29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 wkislnynkiiwtlqdtagnnqkl 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 giysskpsevniaqnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 sytndkililyfnklykkikdnsildmryennkfidisgygsnisingdvylystnrngf 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                             2001-016048/02.
DB; AAA54499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 AA;
                                                                                                                                      Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 144; DB 22; ilarity 100.0%; Pred. No. 7.6e-141; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               99US-0133865.
99US-0133866.
99US-0133867.
99US-0133869.
99US-0133869.
99US-0133873.
                                                                                                                                                                                                  99US-0146192
                                                                                                                                      Middlebrook JL,
                                                                                                                                      Lapenotiere H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT
AAE07894
ID AAE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant of recombinant nucleic acids are expressible in a recombinant of recombinant nucleic acids are expressible in a recombinant botulinum recombinant nucleic acids are expressible in a recombinant of recombinant nucleic acids are expressible to the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
New non toxic polypeptide for delivery of a therapeutic agent
treatment of a CNS disorder comprising a binding domain that
translocates the therapeutic agent into the neuronal cells
                                                                                                                                                                          02-DEC-1999; 99GB-0028530.
07-APR-2000; 2000GB-0008658.
                                                                                                                                                                                                                                                                                                                                   Chimeric - Corynebacterium diphtheriae Chimeric - Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                    Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                               04-DEC-2000; 2000WO-GB04644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                  16-AUG-2001.
                                                                                                                                                                                                                                                                                                     WO200158936-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE07894;
                                                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE07894 standard; Protein; 645 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                          Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 144; DB 22; Length 432; dlarity 100.0%; Pred. No. 7.6c-141; Conservative 0; Mismatches 0; Indels 0;
                                                                                                          Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                        for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN) that translocates the therapeutic CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain of botulinum neurotoxin type F (FRANTEN with translocation Admain of Alentheberia neurotoxin type F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                    umour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; tetanus neurotoxin; TeNT; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                  Chimeric - Corynebacterium diphtheriae
Chimeric - Clostridium tetani.
Chimeric - Clostridium botulinum.
                                                                                            02-DEC-1999;
07-APR-2000;
WPI; 2001-514643/56
                                                                                                                                        04-DEC-2000;
                                                                                                                                                                         16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE07898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07898 standard; Protein; 660
                                                            (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                          Modified clostridial heavy chain fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                        WO200158936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BONT/F) with translocation domain of diphtheria neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                # Wkislnynkiiwtlqdtagnnqkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sytndkililyfnklykkikdnsildmryennkfidisgygsnisingdvyiystnrnqf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           giysskpsevniaqnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg
                                ეე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 44;
                                Sutton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                         99GB-0028530
2000GB-0008658
                                                                                                                                          2000WO-GB04644
                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50pp;
                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                Silman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 144; DB 22;
Pred. No. 1.1e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC substances to neurodegenerative diseases, stroke, epilepsy, brain tumours CC and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain which is a hybrid of botulinum neurotoxin type F (BONT) and tetanus neurotoxin (TeNT) domain II with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translocates the therapeutic agent into the neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that
                                               translocation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Page 46; 50pp;
                                                 of diphtheria neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                                                                        Query Match
Best Local S
Matches 144
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                                        121
                                                        275
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                                                                        61
                                                                                     7
                      giysskpsevniaqnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg
                                                                GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                 Similarity
                                                                                                                          Conservative
                                                                                                                        100.0%; Score 144; DB 22; 100.0%; Pred. No. 1.1e-140; Live 0; Mismatches 0;
                                                                                                                          Indels
                                                                                                                                         Length
                                                                                                                          0;
                                                                                                                         Gaps
                                                        334
                                                                         120
                                                                                          274
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Sequence

660 AA;

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RESULT

AAACOPS

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AC AAECO

XX O1-N

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XX Neul

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OS 
                                                         02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Bacillus stearothermophilus
Chimeric - Influenza virus.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                                                                                                                                                                                                     04-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour; infection; neurodegenerative
superoxide dismutase; SOD; botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuronal cell; binding domain; translocation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE07893 standard; Protein; 685
                                                                                                                                                                                                                                                                                                                                        16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified clostridial heavy chain-superoxide dismutase conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                           2000WO-GB04644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; gene therapy; chi
neurotoxin type F; BONT/F.
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stroke;

#5

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RESULT
AAE07890
ID AAEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapeutic agent to a neuronal cell, which comprises a binding domain C (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino C terminal half of HC, designated as HN), that translocation domain (amino C agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of C a HN domain of a clostridial toxin. Polypeptides of the invention are CC cuseful for the treatment of a disease state associated with neuronal C cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC conjugate to neuronal cells. They are laso useful in gene therapy. The present sequence CC is modified clostridial heavy chain-superoxide dismutase conjugate. This CC conjugate comprises bacterial Mn-superoxide dismutase conjugate. This CC conjugate comprises bacterial Mn-superoxide dismutase conjugate. This CC conjugate bacterial form influenza virus and a neuronal cell-specific CC binding domain from botulinum neurotoxin type F (BoNT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                               Chimeric - Bacillus stearothermophilus.
Chimeric - Corynebacterium diphtheriae.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                 WO200158936-A2
                                                                                                                                                                                                                Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE07890 standard; Protein; 862 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 43; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                              Modified clostridial heavy chain-superoxide dismutase conjugate #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               watch 100.0%; Score 144; DB 22; Local Similarity 100.0%; Pred. No. 1.2e-140; es 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wkislnynkiiwtlqdtagnnqkl 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glysskpsevniaqnndliyngryqnfsisfwvripkyfnkvnlnneytlidcirnnnsg 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE07892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as Hc) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of CC alm domain of a clostridial toxin. Polypeptides of the invention are CC cells. The polypeptide constructs are useful for elivering therapeutic CC cubstances to neuronal cells. They are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC substances to neuronal cells. They are useful to treat disorders of the CC is including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence CC is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from CC modified clostridial heavy chain-superoxide dismutase (MnSOD), from CC constructs and a neuronal cell-cell-cell-cell-cell-domain from diphtheria neurotoxin and a neuronal cell-cell-cell-cell-domain from diphtheria neurotoxin and a neuronal cell-cell-cell-cell-cell-domain from diphtheria neurotoxin type F (BoNT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New non toxic polypeptide for delivery of a therapeutic agent for treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells .
                   superoxide dismutase; SOD; diphtheria neurotoxin; human, botulinum neurotoxin type \mathbf{F}; BoNT/\mathbf{F}.
                                                                           Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
                                                                                                                                                                 Modified clostridial heavy chain-superoxide dismutase conjugate #4.
                                                                                                                                                                                                                      01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                  AAE07892;
                                                                                                                                                                                                                                                                                                                                       AAE07892 standard; Protein; 887 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514643/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROBIOLOGICAL RES AUTHORITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wkislnynkiiwtlqdtagnnqkl 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          862 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 144; DB 22; ilarity 100.0%; Pred. No. 1.4e-140; Conservative 0; Mismatches 0;
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Indels Length 862;

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RESULT 1
AAE07901
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AC AAE0
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic terminal half of HC, designated as HN).
                                                                                                                                                                                                                                                                                                                                                                                                            agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises a mitochondrial leader sequence from human Mn-superoxide dismutase (MnSOD), MnSOD from Bacillus stearothermophilus, linker that can be cleaved by thrombin, translocation domain from diphtheria neurotoxin and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Homo sapiens.
Chimeric - Bacillus stearothermophilus.
Chimeric - Corynebacterium diphtheriae.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1999;
07-APR-2000;
                 AAE07901;
                                            AAE07901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of a Ch
translocates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                           577
                                                                                                                                                                                                                                                 457
                                                                                                                                                      121
                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                           2001-514643/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxic polypeptide for delivery of a therapeutic agent int of a CNS disorder comprising a binding domain that cates the therapeutic agent into the neuronal cells -
                                                                                                                                                                                                                                                                                                                         Similarity
                                            standard;
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000GB-0008658
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                                            Protein;
                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silman N;
                                                                                                                                                                                                                                                                                                            0;
                                            1032 AA
                                                                                                                                                                                                                                                                                                                       Score 144; DB 22;
Pred. No. 1.5e-140;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                       887;
                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                              516
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RESULT 1
AAY93309
ID AAY9
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AC AAY9
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                                                                                                                                                                                                                                     В
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                                                                                                                                        ρy
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                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                   CC The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN) that translocates the therapeutic CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC cells. The polypeptide constructs are useful for delivering therapeutic cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC constitution. They are also useful in gene therapy, brain tumours and infection. They are also useful in gene therapy. The present sequence cc is C. botulinum C2 enterotoxin translocation domain with botulinum CC enterotoxin translocation domain with botulinum CC in the invention of the constructs.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                   Matches
                                  AAY93309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuronal cell; binding domain; translocation domain; stroke; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New non toxic polypeptide for delivery of a therapeutic agreement of a CNS disorder comprising a binding domain the translocates the therapeutic agent into the neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1999;
07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2000; 2000WO-GB04644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
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                                                                                                                                                                          662
                                                                                                                                                                                                                                       602
                                                                                                              722
                                                                                                                                           121
                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                               11
                                                                                                                                                                                                                                                                    1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potulinum
                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                         WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                     GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 48; 50pp; English.
                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotoxin type F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                               1032 AA;
                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99GB-0028530
                              protein; 1059
                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                  Score 144; DB 22;
Pred. No. 1.7e-140;
                                                                                                                                                                                                                                                                                                   Mismatches
                                  A
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                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                  1032;
                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                       120
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AAY93309

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RESULT 1
AAY93312
ID AAY9
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AC AAY9
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                                                                                                                                                                                        В
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                                                                                                                                                                                                                                         Matches 144;
                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                        The present sequence represents a construct of the invention, comprising a mandanese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus stearothermophilus. Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A manganese superoxide dismutase (Mn-SOD) construct
    AAY93312;
                          AAY93312 standard; protein; 1084 AA
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 48-51; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition, concleavable linker to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                   121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                         749
                                                                                                                                         689
                                                                                                                                                                                          629
                                                                                                                                                     61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                    12
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                              1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60
                                                                                      wkislnynkiiwtlqdtagnnqkl 772
                                                                                                                                       glysskpsevnlaqnndllyngryqnfsisfwvripkyfnkvnlnneytildcirnnnsg 748
                                                                                                                                                                                    sytndkililyfnklykkikdnsildmryennkfidisgygsnisingdvyiystnrnqf 688
                                                                                                                                                                                                                                                                                                     1059 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton JM,
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0024282.
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                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hallis B,
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                   Score 144; DB 21;
Pred. No. 1.7e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silman N;
                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                       Indels 0;
                                                                                                                                                                                                                                                             Length 1059;
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                       0;
RESULT 13
AAE07900
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Best Local S
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1998;
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                                                                                                                                                                                                              Local Similarity
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The present sequence represents a construct of the invention, comprisin a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SOD), a Bacillus stearothermophilus Mn-SOD, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as schemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A manganese superoxide dismutase (Mn-SOD) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 57-60; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2000 (first entry)
                                                                                                                       motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       botulinum neurotoxin serotype F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huntington's disease; motor neurone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell;
                                                                                                                                                                                                                                                       774 wkisinynkiiwtlqdtagnnqkl 797
                                                             121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 AA;
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 144; DB 21; illarity 100.0%; Pred. No. 1.8e-140; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98GB-0024282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-GB03699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hallis B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCTC; neuronal
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1084;
                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain is not a HN cC domain of a clostridial neurotoxin and is not a fragment or derivative of CC as HN domain of a clostridial neurotoxin and is not a fragment or derivative of CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC constinction. They are also useful in gene therapy. The present sequence CC is C. botulinum C2 enterotoxin translocation domain with botulinum CC neurotoxin type F (BONT/F) binding domain used in the exemplification of the constitution of the constitution of the invention of the constitution of the constitution of the constitution of the constitution of the invention of the constitution of the constitution of the constitution of the constitution of the invention of the constitution of the constitution of the constitution of the constitution of the invention of the constitution of the constitution of the constitution of the constitution of the invention of the constitution of t
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Best Local Similarity
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07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour; infection; neurodegenerative
botulinum neurotoxin type F; BONT/F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shone CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2000; 2000WO-GB04644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200158936-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. botulinum C2 translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE07900
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocates the therapeutic agent into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROBIOLOGICAL RES AUTHORITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE07900 standard; Protein; 1092
                                              121
                                                                                      722
                                                                                                                                                                            662
      782
                                                                                                                                61
                                                                                                                                                                                                                      \vdash
giysskpsevniaqnndiiyngryqnfsisfwvripkyfnkvnlnneytiidcirnnnsg
                                                                                                   GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-514643/56.
                                                                                                                                                                                                                                                                144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                       1092
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000GB-0008658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding domain; translocation domain; stroke; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99GB-0028530
                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silman N;
                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                           Score 144; DB 22;
Pred. No. 1.8e-140;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain with BoNT/F-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                   Length 1092;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy;
                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                           Gaps
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RESULT 14

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The invention relates to novel vaccines that induce a protective immune CC cresponse against botulinum neurotoxin (BoNT) serotypes A, B, C, D, E, F C and G (BoNTA-BONTG). The vaccine of the invention is novel recombinant CC DNA construct comprising a vector, and at least one nucleic acid CC fragment comprising a C-terminal heavy chain fragment (Hc) from BoNT CC serotypes A-G. In preferred embodiments of the invention, the vector is Serotypes A-G. In preferred embodiments of the invention, the vector use of this vector results in the production of large amounts of a protein cc this vector results in the production of large amounts of a protein cc encoded by a sequence cloned into the replicon. The constructs are used to produce vaccines against botulism. The proteins can also be used as CC diagnostic tools for the diagnosis of botulism. The transformed host cells can be used to analyse the effectiveness of drugs and agents which CC inhibit toxin effects. The vaccine currently used against botulism is CC dangerous and expensive to produce, and contains formalin, which is very painful for the recipient. Also, the vaccine is incomplete, in that only contain the recipient of vaccine of overcomes these problems, as it is easily purified, and available in large quantities. It is also expressed in the lymph nodes of contain the commence had been privinged for rodon usage for the DNA contains the commence had been privinged for rodon usage for
                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY77138;
                                                                                                                                                              expression in yeast. Note:
                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USME-) US MEDICAL RES INST INFECTIOUS DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200002524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY77138 standard; Protein; 432
                                                                                         Sequence
                                                                                                                                              specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin serotypes A-G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-1998;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-160827/14.
 . Similarity 100.88; Conservative
                                                                                                                                              these sequences had been optimised for codon usage for on in yeast. Note: This sequence is not given in the ation, but is decoded from the BONTF Hc DNA sequence gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pushko P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0092416.
99US-0133870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US15570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurotoxin vaccine comprising A-G, is used for inducing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurotoxin serotype F (BoNTF) C-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                  61.1%;
   Score 88; DB; Pred. No. 8.1
   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parker M,
DB 21;
3. 8.1e-83;
3. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dertzbaugh MT,
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immune
                                    Length 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment from botulinum
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith
   0;
     Gaps
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RESULT 1
AAWR 3399
ID AAWR8399
ID AAWR 320
AC AAWR 320
AC AAWR 320
AC Closs
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                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the histidine-tagged C fragment C of Clostridium botulinum (202F strain) type F neuroboxin, encoded by a DNA sequence (see ANV3053) in plasmid pEFHisb. This vector can be used to express BotC soluble C fragment in Escharichia coli host cells, with the recombinant C fragment being purified on an affinity column. The invention relates to recombinant proteins certain derived from C. botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin contamination. Preferred hosts for production of recombinant coxins are E. coll, insect cells and yeast cells. The recombinant toxins are used as immunogens for the production of waccines and antitoxins that are useful in the treatment of humans and animals at risk of intoxication with clostridial toxin.
                                                                                                                                                        Query Match
Best Local S
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat humans and other animals at risk of intoxication with clostridial toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9808540-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium botulinum type F toxin C fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW68399 standard; Protein; 448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-230234/20.
N-PSDB; AAV30593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thalley BS, Williams JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  botulism; BotF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antitoxin; vaccine; neurotoxin; toxin F; intoxication; immunogen;
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                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                    h 18.1%; Score 26; DB 19;
Similarity 100.0%; Pred. No. 1.5e-18;
26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    448 AA;
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Search completed: August 15, 2002, 11:12:26 Job time: 318 sec

P92849 P33882 013777 P47256 Q21824 P34128 P34128 P35387 P35387 P36186

bungarus mu salmonella mycoplasma caenorhabdi erwinia bothriechis

4 buchnera ap 7 hypoderma 1 6 giardia lam 7 giardia lam 9 methanococc

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Total number of hits satisfying chosen parameters:
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"Cleavage of members of the synaptobrevin/YAMP family by types D and be botulinal neurotoxins and tetanus toxin.";
J. Biol. Chem. 269:12764-12772(1994).

1. Biol. Chem. 269:12764-12772(1994).

1. Biol. Chem. 269:12764-12772(1994).

1. Biol. Chem. 279:12764-12772(1994).

1. Biol. Chem. 289:12764-12772(1994).

1. Biol. Chem. 289:12764-12772 AU D. PRESYNAPTIC NEURONS. IT INTERNALIZED TRANSPORT UP THE XNON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENNOPERIVAN THAT CATALYZES THE HYDROLYSIS OF THE 58-GLN-|-LYS-59-BOND OF SYNAPTOBREVINS-1 AND -2.

1. CATALYTIC ACTIVITY: Linited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or Syntaxin. No
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MEDLINE-94013372; PubMed-8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 2388;
MEDLINE-93012902; PubMed=1398040;
East A.K., Richardson P.T., Allaway D., Collins M.D.,
Roberts T.A., Thompson D.E.;
"Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.";
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p30996;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BONT/F)
(Bontoxilysin F).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-64 FROM N.A.
STRAIN-HOBBS FT10;
MEDLIANE-94297488; PubMed-7764998;
East A.K., Collins M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium botulinum Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                      IDENTIFICATION OF SUBSTRATE.

MEDLINE=94230352; PubMed=8175689;
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Y010_MYCGE
TDX1_CAEEL
NGF_BUNMU
PLSC_SALTY
Y276_BUCAI
HYPA_HYPLI
TP11_GIALA
TP12_GIALA
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Database :

Score

Query Match Length

SUMMARIES

RK20_ASTLO

CFTR_MACMU
CFTR_CAVPO
Y426_METJA
Y262_HELPY
YPBH_BACSU
TSA1_CANAL
VATD_AERPE
CYOC_BUCAI

YP78_CAEEL CYB_AGKCO CYB_AGKHA

BXE_CLOBO
BXE_CLOBO
BXE_CLOBU
BXA_CLOBO
BXB_CLOBO
BXB_CLOBO
BXA_CLOBO
MURE_RICPE
VGLC_HSVMB
VGLC_HSVMB
VGLC_HSVMG
RRBL_YEAST
POLG_EMCVB
POLG_EM

Post-processing: Listing first 45 summaries

SwissProt_40:*

DB seq length: 0
DB seq length: 2000000000

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Title: Perfect score:

US-'08-981-087A-2 144

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OM protein - protein search, using sw model

August 15, 2002, 11:24:37;

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01-JUL-1993 (Rel. 2
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                                        STRAIN-BELUGA;

STRAIN-BELUGA;

MEDLINE=92181428; PubMed=1543481;

Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;

"Sequences of the botulinal neurotoxin E derived from C1

botulinum type E (strain Beluga) and Clostridium butyric

ATCC 43181 and ATCC 43755).";

183:107-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M92906; I
EMBL; S73676; I
EMBL; X70820; GEMBL; X70816; GEMBL; X70816; GEMBL; T0845; 3
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  SEQUENCE
                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                    Clostridium botulinum
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InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01742; Peptidase_W77; 1.
PRINTS; PR00760; BONTOXILYSIN.
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MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detected action on small molecule substrates.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
FORMATION AND TOXIN BINDING, RESPECTIVELY.
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E; PS00142;
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BOTULINUM NEUROTOXIN F, HEAVY-CHA
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                                                                                              modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Gimenez J.A., Dasgupta B.R.;
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                                                                                                                                                                                                     the
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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J. Biol. Chem. 269:1617-1620(1994).
-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Botulinum neurotoxins serotypes COOH-terminal peptide bonds."; FEBS Lett. 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schiavo G., Santtuci A., Dasgupta B.R., Benfenati F., Wilson M.C., Montecucco C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94124495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94063091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochimie 72:213-217(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurotoxin
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Schmidt J.J., Sat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION OF SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botulinum neurotóxin type E fragmented with endoproteinase Lys-C"
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                                                                                                                                                                                                                                                                                                                                                                                              neuroexocytosis apparatus, synaptobravins, SNAP25 or syntax detected action on small molecule substrates. SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL AC WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANN FORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT
BOTULLIUM NEUROPOXIN: TYPES A, B, C1, D, E, F, AND G.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 BOND IN SNAP-25.
CATALYTIC ACTIVITY: Limited hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERIDASE THAT CATALYZES THE HYDROLYSIS OF THE 180-ARG-|-ILE-TRANSPORT AND ARG-|-ILE-TRANSPORT ARG-|-ILE-TRANSPORT AND ARG-|-ILE-TRANSPORT A
                                                                                                                                                                                                   European
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R., Niemann H
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                                                                                                                                                                           non-profit
                                                                                                                                                                         Bioinformatics Institute. The profit institutions as long
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Sathyamoorthy V., Dasgupta B.
o acid sequences of botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204:657-667(1992).
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RESULT BYE CLOSE OF THE CLOSE O
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01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BONT/E)
(Bontoxilysin E)
Clostridium butyricum.
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CHAIN
METAL
ACT_SI
                                           MEDLINE-91237316; PubMed-203376; Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 43181, AND ATCC 43755;
MEDLINE-92181428; PubMed-1543481;
MEDLINE-92181428; PubMed-1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Sequences of the botulinal neurotoxin E derived from Clostridium
botulinum type E (strain Beliga) and Clostridium butyricum (strains
botulinum type E (strain Beliga) and Clostridium butyricum (strains
ATCC 43181 and ATCC 43755).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium Clostridium.
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase, M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
   SEQUENCE OF 1-48
                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 183:107-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1492;
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                                                                                                                                                                                                                                       SEQUENCE OF 1-251 FROM N.A.
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; JH0257; JH0257.

; S08575; S08575.

; S18111; S18111.

; S21178; S21178.

; P10845; 3BTA.
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Conservative
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100.0%; Pred. No.
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R -5 G (IN REF. 2).

C -> S (IN REF. 2 AND 3)

R -> A (IN REF. 2).

I -> L (IN REF. 2).

FE -> LQ (IN REF. 2).

R -> A (IN REF. 2).

R -> A (IN REF. 2).

N -> NN (IN REF. 2).

N -> NN (IN REF. 2).
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BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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/o. 0.0012;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    group; Clostridiaceae;
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Q45894; p77780;
Q45894; p77780;
Q1-MAR-2002 (Rel. 41, Created)
Q1-MAR-2002 (Rel. 41, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Bottlinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
Bottlinum neurotoxin A, 1
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ACT_SITE
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"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
PASEB J. 2:A1750-A1750(1988).

-i- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_Wipeptdse.
Pfam; PF01742; Peptidase. W27; 1.
PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X62088; CAA43998.1; -. EMBL; X53180; CAA37321.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1
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PIR; S16145; S16145.
HSSP; P10845; 3BTA.
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CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the catalytic activity: Lynaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

SUBCELLAURAL LOCATION: Secreted.
MISCELLAURACUG: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

SIMILARTY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 100.0%;
11; Conservative
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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K -> M (IN REF. 2).

W; 8171B5B2C2312857 CRC64;
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0.0012;
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TRANSMEM
                 DISULFID
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                                                                                                                                             PROSITE; PS
Neurotoxin;
                                DISULFID
                                                               ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Willems A., East A.K., Lawson P.A., Coll
"Sequence of the gene coding for the new
botulinum type A associated with infant
other clostridial neurotoxins.";
                                                 METAL
                                                                                                                                                                              ProDom; PD001963;
                                                                                                                                                                                             PRINTS; PR00760;
                                                                                                                                                                                                              InterPro; IPR000395; Bontoxilysin.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                  MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97016817; PubMed=8863443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-65 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroexocytosis apparatus, synaptobravins, SNAP25 or s detected action on small molecule substrates. SUBUNIT: Disulfide-linked heterodimer of a light chain heavy chain (H) (By similarity). SUBCELLULAR LOCATION: Secreted. MISCELLANEOUS: There are seven antigenically distinct bottlinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e encoding the nontoxic nonhemagglutinin component.";

J. Syst. Bacteriol. 46:1105-1112(1996).

FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    failure (By similarity).
CATALYTIC ACTIVITY: Limited hydrolysis of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR.
                                                                                                                                                                                                                                                            X73423; CAA51824.1;
X87974; CAA61234.1;
P10845; 3BTA.
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                                                                                                                                                                                                                                                M27.002
                                                                                                                                                                                                                                                                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                          PS00142; ZINC_PROTEASE; FALSE_NEG.
in; Transmembrane; Hydrolase; Metalloprotease;
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222
223
226
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1279
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A.K., Lawson P.A.
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                           BY SIMILARITY.

BOTULINUM NEUROTOXIN A, LIGHT
BOTULINUM NEUROTOXIN A, HEAVY
BOTULINUM NEUROTOXIN A, HEAVY
ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).
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               SIMILARITY
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                                              (BY SIMILARITY)
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-- comparison with
                                                                           N A, LIGHT-CHAIN.
N A, HEAVY-CHAIN.
Y SIMILARITY).
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Best Local
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P10844; P10843;
01-JUL-1989 (Rel. 11, 0
01-JUL-1993 (Rel. 26, I
01-MAR-2002 (Rel. 41, I
Botulinum neurotoxin ty
                                 MEDLINE=93054694;
Schiavo G., Rossott
                                                                                                                                                            "Botulinum neurotoxin type B (strain similarity with tetanus toxin.";
Biochimie 70:811-817(1988).
                                                                                                                                                                                                                                                                                                                                                                 encoding the type B neurotoxin and determinate nucleotide sequence.";
Appl. Environ. Microbiol. 58:2345-2354(1992).
[2]
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SEQUENCE
                                                                                                 MEDLINE-85197963; PubMed-3888113; Schmidt J.J., Sathyamoorthy V., Dasgupta B "Partial amino acid sequences of botulinum
                                                                                                                                                                                                                                                                                  SEQUENCE OF 633-993 FROM STRAIN=NCTC 7273; MEDLINE=94013372; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92384550;
Whelan S.M., Elmon
Minton N.P.;
                Schiavo G., Rossetto O., Santucci A., Da: "Botulinum neurotoxins are zinc proteins J. Biol. Chem. 267:23479-23483(1992).
                                                                                          "Partial amino E.";
                                                                                                                                          SEQUENCE OF 1-16
                                                                                                                                                                                                                                          Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal specific identification of neurotoxin types B, E, J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                    Szabo E.A.,
                                                                                                                                 STRAIN=OKRA;
                                                                                                                                                                                                    MEDLINE=89000987; PubMed=3139097;
                                                                                                                                                                                                                                                                                                                          Submitted (APR-1992)
                                                                                                                                                                                                                                                                                                                                             STRAIN-NCTC
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                                                                                Biochem.
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9; Conserv
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 SUBSTRATE
                                                PubMed=1429690
                                                           ZINC-PROTEASE
                                                                                                                                                                                                                                                                                   PubMed=8408542;
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Last annotation update)
type B precursor (EC 3.4.24.69) (BONT/B)
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149279 MW; 5DA041
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                                                                              238:544-548(1985)
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                                 Dasgupta
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. 0.17;
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R
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                                                                                                   neurotoxins
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R.,
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, and F.";
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EMBL; Z11934; CAA77991.1; ...
EMBL; Z10817; CAA50148.1; -..
PIR; S07128; S07128.
PIR; S07128; S07128.
PIR; S08562; S08562.
PIR; S08562; S08573.
PIR; S08573; S08573.
PIR; S08574; S08574.
PIR; A88940; A48940.
HSSP; P10845; 3BTA.
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CONFLICT
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METAL
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-I- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, symaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.
-I- SUBUNIT: DISULFIDE-LINED HYTEROIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.
-I- MISCELLULAR LOCATION: Secreted.
-I- MISCELLULAR LOCATION: SECRETIVE A, B, Cl, D, E, F, AND G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
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                                                                                           NNSGWKIS 124
                                                                                                                                       Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Hydrolase; Metalloprotease; Zinc.
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                           AΑ;
                                                                                                                                                          5.6%;
                                                                                                                                                                                                                                                        150670
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R -> G (IN REF. 2)
A -> S (IN REF. 2)
S -> R (IN REF. 2)
S -> R (IN REF. 4)
O MW; D21746F2222
                                                                                                                                                                                                                                                                                                                                              BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
T -> M (IN REF. 4).
                                                                                                                                       Score 8; DB;
; Pred. No. 1.
0; Mismatches
                                                                                                                                                                                                                                                     D21746E2C024DF43 CRC64;
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o. 1.9;
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                                                                                                                                    0,:
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                                                                                                                                    0;
RESULTS 6

RALLCLOBO STANDARD; PRT; 1295 AA.

DEMALCLOBO STANDARD; PRT; 1295 AA.

AC P10845; P10839; P01561;

DEMALCLOBO STANDARD; PRT; 1295 AA.

AC P10845; P10839; P01561;

DE P10845; P10839; P01561;

DE P10845; P10839; P01561;

DE P10845; P10839; P01561;

DE ROCKSLIVSIA A, 1607031 (COTOTAINS BEDLIAMM NEWTOTOXIA A, 119ht-
DE CHAIN; BOULLIAMM REUTOXIAI A, heavy-chain).

DE ROCKSLIVSIA A, 1607031 (COTOTAINS BEDLIAMM SEVENCE).

CHECKETI, FIRMICLUSS; BACILLUS/CLOSTRIDIUM TOWN.

RESULTING-90264400; PUDMED-2169960;

RESULTING-90264400; PUDMED-216990;

RESULTING-90264400; PUDMED-2169960;

RESULTING-90264400; PUDMED-216990;

RESULTING-90264400; PUDMED-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.; "Organization and phylogenetic interrelationships of genes encoding "components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component."; Int. J. Syst. Bacteriol. 46:1105-1112(1996).
                                                                                                                                                                                                                                                                                                                        Fujita R., Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.; "Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins."; FEBS Lett. 376:41-44(1995).
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"The complete sequence of bottninum neurotoxin type A and comparison
with other clostridial neurotoxins.";
"In Biol. Chem. 265:9153-9158(1990)."
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e C.C., Atkinson T., Melling J., Minton N.P.;

complete amino acid sequence of the Clostridium botulinum type
ptoxin, deduced by nucleotide sequence analysis of the encoding
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MEDLINE-85285016; Pub
Shone C.C., Hambleton
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Binz T., Blasi J., Y
Jahn R., Niemann H.;
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MEDLINE=98455071; Publ
Lacy D.B., Tepp W., Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Crystal structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schiavo G., Santtuci A., Dasgupta B.R., Benfenati F., Wilson M.C., Montecucco C.
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the
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                                                                                                                                                                                                                                                    Struct. Biol. 5:898-902(1998).

FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
           heavy chain (H).
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
PHARMACEUTICAL: Available under the name BOTOX(R) (Allergan)
the treatment of strabismus and blepharospasm associated wit
dystonia and cervical dystonia. Also used for the treatment
hemifacial spasm and a number of other neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ne C.C., Hambleton P., Melling J.;
activation of Clostridium bottulinum type A neurotoxin by
purification of two tryptic fragments. Proteolytic actio
COOH-terminus of the heavy subunit destroys toxin-bindin
                                                                                                                                                  neuroexocytosis apparatus, synaptobravins, SN detected action on small molecule substrates. SUBUNIT: Disulfide-linked heterodimer of a li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxicity."
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PubMed=2126206;
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266:142-151(1988).
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30-CT-2001 (Rel. 40, Last annotation update)
Probable UDP-N-acetylmuramoylalanyl-DD-dlamyl-2,6-diaminopimelate--D-alanyl-D-alanyl-ligase (EC 6.3.2.15) (UDp-MurNAc-pentapeptide
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3BTA; 01
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                  (D-alanyl-D-alanine-adding
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261
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HEAVY-CHAIN.
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Matches
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Best Local :
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P22650;
01-AUG-1991
01-AUG-1991
16-OCT-2001
  Secretory (GA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
Pfam; PP01225; Mur_ligase; 1.
Pfam; PP02875; Mur_ligase_C; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.
NP_BIND 106 112 ATP (POTENTIAL).
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Andersson J.O.,
Sicharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
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nes 7; Conser
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                                            (Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 40, Last annotation updat)
lycoprotein GP57-65 precursor (A
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                                       precursor (A antigen) (Glycoprotein
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P33500;
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01-FBB-1994 (Rel. 28, Last sequence update)
30-ANY-2000 (Rel. 39, Last annotation update)
Secretory glycoprotein GP57-65 precursor (A antigen) (Glycoprotein
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                                    Marek's disease herpesvirus (strain RB-1B) (MDHV) Viruses; dsDNA viruses; no RNA stage; Herpesviric Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=33707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marek's disease herpesvirus (strain bc-1) (MDHY).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10387;
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Pfam; PF02124; Marek_A; 1.
PRINTS; PR00675; MAREKSGPA.
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100.0%; Pr
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POTENTIAL.

SECRETORY GLYCOPROTEIN GP57-65.

SECRETORY GLYCOPROTEIN GP57-65.

NEMBRANE ANCHOR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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P22651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence of the Marek's disease virus (MDV) RB-1B A antigen gene and the identification of the MDV A antigen as the herpes simplex virus-1 glycoprotein C homologue.";
Virus Res. 12:371-382(1989).
-!- FUNCTION: MAY PLAY AN IMMUNOEVASIVE ROLE IN THE PATHOGENESIS OF MAREK'S DISEASE. IT IS A CANDIDATE FOR CAUSING THE EARLY-STAGE IMMUNOSUPPRESSION THAT OCCURS AFTER MDHY INFECTION.
-!- SUBCELLULAR LOCATION: PREDOMINANTLY SECRETED, BUT A SMALL AMOUNT OF MATURE GP57-65 IS ANCHORED IN THE PLASMA MEMBRANE OR HELD BY
    between
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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SIGNAL
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Binns M.M., Ross |
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                                                      OTHER INTERACTIONS.
SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN C FAMILY.
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SIMILARITY: BELONGS TO
SWISS-PROT entry is copyright. It is produced through a seen the Swiss Institute of Bioinformatics and the EMBL
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Last annotation updat
n GP57-65 precursor (A
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POTENTIAL.
SECRETORY GLYCOPROTEIN GP57-65.
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SEQUENCE
                                                                                                                            Coussens P.M., Velicer L.F.;

"Structure and complete nucleotide sequence of the Marek's disease herpesvirus gp57-65 gene.";

J. Virol. 62:2373-2379(1988).

-I- FUNCTION: MAY PLAY AN IMMUNOEVASIVE ROLE IN THE PATHOGENESIS OF MAREK'S DISEASE. IT IS A CANDIDATE FOR CAUSING THE EARLY STAGE IMMUNOSUPPRESSION THAT OCCURS AFTER MOHY INTECTION.

-I- SUBCELLULAR LOCATION: PREDOMINANTLY SECRETED, BUT A SMALL AMOUN OF MATURE GP57-65 IS ANCHORED IN THE PLASMA MEMBRANE OR HELD BY
  entities requires a or send an email to
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-88230597; PubMed=2836620;
                                                                                                                                                                                                                                                                                    Marek's disease herpesvirus (strain GA) (MDHV)
Viruses; dsDNA viruses, no RNA stage; Herpesvi
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, C
01-JAN-1990 (Rel. 13, I
30-MAY-2000 (Rel. 39, I
Secretory glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                  use by non-profit institutions as long modified and this statement is not removed
                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                      between
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                                                                                                                                                                                                                                                                          NCBI_TaxID=10388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001654; Marek_A.
Pfam; PF02124; Marek_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D90001; BAA14052.1; -.
                                                                                                                                                                                                                                                                                                                                    (GA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                        SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN C FAMILY
                                                                                                                     OTHER INTERACTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A22818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNISING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA,
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91
1100
1120
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212
354
400
429
423
56088
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                                                                                                                                                                                                                                                                                                                                 13, Createa)
13, Last sequence update)
39, Last annotation update)
cotein GP57-65 precursor (A a
           license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%;
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POTENTIAL.
SECRETORY
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Pred.
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N-LINKED (GLCNAC. . .) (P
4393C56AA779340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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D (GLCNAC...) (POTE
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9
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SIGNAL
CHAIN
TRANSMEM 46
CARBOHYD 4
CARBOHYD 9
CARBOHYD 11
CARBOHYD 11
CARBOHYD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRBI_YEAST STANDARD; PRT; 511 AA 004225; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat Ribosome assembly protein RRB1. RRB1 OR YMR131C OR YM9553.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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CARBOHYD
              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      Curr.
                                                                                                                                                                                                                                                 ribosome assembly.";
Curr. Biol. 11:1885-1890(2001)
                                                                                                                                                                                                                                                                                            Schaper S., Fromont-Racine M., Linder P., de la Cruz J., Namane A., Yaniv M.;
                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE=21585391; PubMed=11728313;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C / AB972;
Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C / ABS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
EMBL; Z48622; CAA88556.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M20001; AAA46114.1; PIR; A28843; VGBEMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 SNISING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 SNISING 48
                                                                                                                                                                                                                                                                             yeast homolog of chromatin assembly factor 1 is involved in early
                                                                                                                               precursor trnn.
SUBUNIT: Associates with ribosomal protein L3.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                   FUNCTION: Involved
                                                                                                                                                                                        FUNCTION: Involved in regulation of L3 expression and stability and plays a role in early 60S ribosomal subunit assembly. May be required for proper assembly of preribosomal particles during early ribosome biogenesis, presumably by targeting L3 onto the 35S
                                                                                         SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR001654; Marek_A.
pF02124; Marek_A; 1.
S; PR00675; MAREKSGPA.
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7; Conser
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465
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505 AA;
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465 491
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428
56809 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.9%; 5u.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e; Signal.

POTENTIAL.

POTENTIAL.

SECRETORY GLYCOPROTEIN GP57-65.

MEMBRANE ANCHOR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 AA
                                     (See http://www.isb-sib.ch/announce/
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oved. Usage by an
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                                                                            restrictions
                                                    and for
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                       POLG_EMCVB STANDARD; PRT; 2292 AA.

P17593;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-AUG-1990 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C
(EC 3.4.22.28) (PTotease 3C) (P3C); RNA-directed RNA polymerase P3D

(EC 2.7.7.48)]
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                             MEDLINE-89243189; PubMed-2541543;
MEDLINE-89141543;
Finn H.M., Yoon J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; S0004738; RRB1.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 4.
PRINTS; PR00330; GPROTEINE
                                                                   EMBL; M22457; AAA43033.1; ALT_SEQ.
PIR; B31473; GNNYEB.
HSSP; P12296; 2MEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
        InterPro; IPR000605; RNA_helicase
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; Rhv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMCVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00320; GPROTE SMART; SM00320; WD40; 4
                                            MEROPS; C03.009;
MEROPS; U29.001;
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=12105;
                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                              Encephalomyocarditis virus (strain emc-b nondiabetogenic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                   PTM: SPECIFIC ENZYMATIC CLEAVAGES IN TITE TO THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGDVYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
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404 W
455 W
510 W
57261 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9%; 5cc
100.0%; Pr
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Pred. No.
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WD 2.
WD 3.
WD 4.
1D18CE3C60BAFF30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                               noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                   no DNA stage; Picornaviridae
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EMBL outstation -
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in no way
commercial
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PF00073; rhv;

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PRESULT POLICE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein (Contains: Coat proteins VP1 TO VP4; (P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polyprotein 1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLG_EMCVD
P17594;
01-AUG-1990
01-FEB-1996
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                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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Pfam; PF00910; RNA_helicase;
Polyprotein; Coat protein; Co
RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89243189; PubMed-2541543; Bae Y.S., Eun H.M., Yoon J.W.; "Genomic differences between the
                                      EMBL; M22458; AAA43034.1; PIR; A31473; GNNYED.
                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                variants of encephalomyocarditis Virology 170:282-287(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Encephalomyocarditis virus (strain emc-oviruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMCVD
                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                          <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=12106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 LQDTAGN 140
                                                                                                                                                                                                                                                              FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE. SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF PROTEINS VP1, VP2, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, VP3, AND VP4.

PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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                                                                                                s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
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RNA_helicase; 1.
oat protein; Core
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COAT PROTEIN VP2 (BETA).
COAT PROTEIN VP3 (GAMMA).
COAT PROTEIN VP1 (ALPHA).
COAT PROTEIN P2A (G).
CORE PROTEIN P2B (I).
CORE PROTEIN P2B (F).
CORE PROTEIN P3A.
GENOME-LINKED PROTEIN VPG (I)
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RNA-DIRECTED RNA POLYMERASE P3D
MYRISTATE (BY SIMILARITY).
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Matches 7
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MEDLINE-95327656; PubMed-7604004;

Li D., Noyes I., Shuler C., Milo G.E.;

"Cloning and sequencing of CATR1.3, a l
tumorigenic conversion.";

tumorigenic conversion. U.S.A. 92:6409-1

Proc. Natl. Acad. Sci. U.S.A. 92:6409-1
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16-OCT-2001
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Pfam; PF00073; rhv; 3.

Pfam; PF00680; RNA_dep_RNA_pol; 1.

Pfam; PF00910; RNA_helicase; 1.

Polyprotein; Coat protein; Core protein;
                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                      CATR tumorigenic
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InterPro; IPR001205; RNA_pol_P3D.
                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 92:6409-6413(1995).
                                                                                                                                                                                                                    NCBI_TaxID=9606;
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PICORNAIN 3C (P22).
RNA-DIRECTED RNA POLYMERASE P3D (I
MYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).
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PROTEASE (POTENTIAL).
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T PROTEIN VP3
T PROTEIN VP1
PROTEIN P2A
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E PROTEIN P2C
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(CATR1.3).
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(BETA).
(GAMMA).
(ALPHA).
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BC3667C059114CF3

CRC64;

Search completed: August 15, 2002, 11:24:38	Qy 74 QNNDII 79 Db 15 QNNDII 20	Best Local Similarity 100.0%; Pred. No. 24; Matches 6; Conservative 0; Mismatches
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                        Score
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1. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

3. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

4. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

5. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

6. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

7. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*

7. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*

8. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
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Gapop 60.0 , Gapext 60.0
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1 VENYTOMISISDYINKWIEV.....ITQNSNFLNINQQRGVYQKP 144
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Copyright (c) 1993 - 2000 Compugen Ltd
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Immunogenic type F
Immunogenic type F
Synthetic botulinu
Botulism toxin hea
Botulism toxin hea
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Modified clostridi
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C. botulinum C2 tr
A manganese supero
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
7	7	7	7	8	80	œ	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	Ħ	11	15	15	15	15	15	27	69	144	144
4.9	4.9	4.9	4.9				7.6		7.6	7.6	7.6	7.6		7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6		10.4	10.4	10.4	10.4	10.4	٠		00.	100.0
206	196	196	20	473	449	449	1296	1092	1067	847	837	462	462	445	438	438	438	437	435	434	432	415	382	233	452	451	449	449	419	448	660	1092	1084
21	15	15	16	19	22	21	17	21	21	22	21	19	17	19	21	19	17	22	22	22	21	22	21	21	19	19	22	21	22	19	22	22	21
AAY77144	AAR55343	AAR43986	AAR64982	AAW68400	AAB04167	AAY77139	AAR95010	AAY93310	AAY93307	AAB04081	AAY77140	AAW68390	AAR95009	AAW68391	AAY77134	AAW68389	AAR95008	AAB04088	AAB04090	AAB04089	AAY77142	AAB04083	AAB36303	AAY77143	AAW68396	AAW68395	AAB04094	AAY77137	AAB04095	AAW68399	AAE07898	AAE07900	AAY93312
Botulinum neurotox	Sequence of envelo	p15e Protein. Hum	MMLV plsE Clq bind	Clostridium botuli	Botulism toxin hea	Synthetic botulinu	C. botulinum type	A manganese supero	A manganese supero	Botulism toxin hea	Native botulinum n	Clostridium botuli	Type A neurotoxin	Clostridium botuli	Synthetic botulinu	Clostridium botuli	Type A neurotoxin	toxin	Botulism toxin hea	Botulism toxin hea	Native botulinum n	Botulism toxin C f	BoNT/A prototoxin	Botulinum neurotox	Clostridium botuli	Clostridium botuli	Botulism toxin hea	Synthetic botulinu	Botulism toxin hea	Clostridium botuli	Modified clostridi	=	A manganese supero

ALIGNMENTS

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RESULT
AAW09016
Claim 5; Page 18-19; 37pp; English.
                                     Immunogenic type {\tt F} botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                        WPI; 1997-065467/06.
                                                                                           Elmore MJ, Mauchline ML, Minton NP,
                                                                                                               (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                      12-JUN-1995;
                                                                                                                                                          12-JUN-1996;
                                                                                                                                                                                27-DEC-1996.
                                                                                                                                                                                                    WO9641881-A1.
                                                                                                                                                                                                                        Clostridium botulinum type F strain Langeland.
                                                                                                                                                                                                                                              Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism.
                                                                                                                                                                                                                                                                  Immunogenic type F botulinum toxin polypeptide (aa992-1135).
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                                                                                                                                                                                                                                                                                                             AAW09016;
                                                                                                                                                                                                                                                                                                                                 AAW09016 standard; Protein; 144 AA
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                                                                                                                                      95GB-0011909.
                                                                                                                                                           96WO-GB01409.
                                                                                             Pasechnik VA;
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Novel polypeptides (AAW09014-17) respectively comprise amino acids

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RESULT AAWO9014
ID AAWO9014
AC AAWO
AC AAWO
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                                A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278) of a type F botulinum neurotoxin (BONT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be
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a Venezuelan equine encephalitis virus (VEE) replicon vector. Use of this vector results in the production of large amounts of a protein encoded by a sequence cloned into the replicon. The constructs are used to produce vaccines against botulism. The proteins can also be used as diagnostic tools for the diagnosis of botulism. The transformed host cells can be used to analyse the effectiveness of drugs and agents which
                                                                                                                  The invention relates to novel vaccines that induce a protective immune response against botulinum neurotoxin (BoNT) serotypes A, B, C, D, E, F and G (BoNTA-BoNTG). The vaccine of the invention is novel recombinant DNA construct comprising a vector, and at least one nucleic acid fragment comprising a C-terminal heavy chain fragment (Hc) from BoNT serotypes A-G. In preferred embodiments of the invention, the vector is a Venezuelan equine encephalitis virus (VEE) replicon vector. Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Botulinum neurotoxin; heavy chain; BoNT; serotype F; C-terminal fragment; Venezuelan equine encephalitis VEE; botulism; vaccine; diagnosis; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                               inducing
                                                                                                                                                                                                                                                                                                                                                                                                        comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144; DB 18;
No. 3.9e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ž
                                                                                                                                                                                                                                                                                                                                                                                  an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dertzbaugh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BONTF) C-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                  g a fraq
immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                        fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus replicon;
                                                                                                                                                                                                                                                                                                                                                                                  response
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                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                  against
                                                                                                                                                                                                                                                                                                                                                                                                        botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Query Match
                                                                                                                                                                                                                                                    12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibit toxin effects. The vaccine currently used against botulism is dangerous and expensive to produce, and contains formalln, which is very painful for the recipient. Also, the vaccine is incomplete, in that only 5 of the 7 serotypes are represented in the formulation. The novel vaccine of overcomes these problems, as it is easily purified, and available in large quantities. It is also expressed in the lymph nodes for a better immune response. Sequences AAV77139 represent synthetic BONT Hc fragments used in the present invention. The DNA encoding these sequences had been optimised for codon usage for expression in yeast. Note: This sequence is not given in the specification, but is decoded from the BONTF Hc DNA sequence given on pages 45-46.
                                                                                                                                                                                                                                                                                                                                                12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Clostridium botulinum.
New nucleic acids encoding the carboxy-
the heavy chain of botulinum neurotoxin
                                                                        N-PSDB; AAA54490
                                                                                                                                      Smith LA,
                                                                                                                                                                                 (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-2000; 2000WO-US12890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200067700-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulism; toxin; neurotoxin; heavy chain; recombinant expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB04096 standard; Protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 tdksitqnsnflningqrgvyqkp 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                           2001-016048/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                      Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                    99US-0133865.
99US-0133866.
99US-0133867.
99US-0133869.
99US-0133869.
99US-0133873.
                                                                                                                                                                                                                            99US-0146192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 144; DB 21; 100.0%; Pred. No. 3.9e-147;
                                                                                                                                      Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                   Lapenotiere
or amino-terminal portions of serotype A-G, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                     of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB04103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                               12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coll or Pichlia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bottlism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain which consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BNT) can be used in recombinant chain of botulinum neurotoxin (BNT) can be used in recombinant
(USSA ) US ARMY
                                                                                                                                                                 12-MAY-2000;
                                                                                                                                                                                               16-NOV-2000.
                                                                                                                                                                                                                                WO200067700-A2
                                                                                                                                                                                                                                                               Clostridium botulinum.
                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                               Botulism; toxin;
                                                                                                                                                                                                                                                                                                                                                                              Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB04103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB04103 standard; Protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 9b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine against botulism
                                                                                                                                                                                                                                                                                                                 intection
                                                                                                                                                                                                                                                                                                                                recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 tdksitqnsnflningqrgvyqkp 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 vgcndtryvgiryfkvfdtelgkteietlysdepdpsilkdfwgnyllynkryyllnllr 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               տ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGCNDTRYVGIRYFKVFDTELGKTELETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                 2000WO-US12890
                                               99US-0133865.
99US-0133866.
99US-0133867.
99US-0133869.
99US-0133873.
                                    99US-0146192
   MEDICAL RES
                                                                                                                                                                                                                                                                                                                            neurotoxin; heavy chain; recombinant expression;
or; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 144; DB 22; 100.0%; Pred. No. 3.9e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
   & MATERIAL COMMAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT A AAEC/PA AAEC/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botulism neurotoxins are translated as a single 150 kDa polypeptide C chain and then posttranslationally nicked, forming a dichain C consisting of a 100 kDa heavy chain and a 50 kDa light chain which C consisting of a 100 kDa heavy chain and a 50 kDa light chain which C cremain linked by a disulfide bond. Nucleic acids encoding the C carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy C chain of botulinum neurotoxin (BoNT) can be used in recombinant C expression vectors and expressed in transformed cells to produce C peptide antigens useful for eliciting an immune response to give C protective immunity against botulinum neurotoxin, which causes C botulism. The nucleic acids are expressible in a recombinant C organisms such as Escherichia coli or pichia pastoris. The use C of recombinant nucleic acids are advantageous since it eliminates C the need to culture large quantities of hazardous toxin-producting C bacterium. Production yield from the genetically engineered product C is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                    Chimeric - Corynebacterium
Chimeric - Clostridium botu
   02-DEC-1999;
                                                                                                                                                                                                                                                                                                                     Neuronal cell; binding domain; translocation domain; stroke tumour; infection; neurodegenerative disease; gene therapy; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                            04-DEC-2000;
                                                                                                                     16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE07894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 18b; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine
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                                                                                                                                                                              WO200158936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE07894 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding the carboxy-
the heavy chain of botulinum neurotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-016048/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vfnytqmisisdyinkwifvtitnnrlgnsriyingnlideksisnlgdihvsdnilfki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   against botulism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                            2000WO-GB04644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA,
   99GB-0028530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                       botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 144; DB 22;
Pred. No. 3.9e-147;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lapenotiere H;
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serotype A-G, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                              stroke;
                                                                                                                                                                                                                                                                                                                                                   chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino CC agent into the neuronal cell, where the translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC constluding neurodegenerative diseases, stroke, epilepsy, brain tumours CC and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is CC constructed by fusing the binding domain of botulinum neurotoxin type F CC (BONT/F) with translocation domain of diphtheria neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-2000; 2000GB-0008658
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROBIOLOGICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-514643/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton JM,
645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORITY
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Query Match
Best Local S
Matches 144
                                                       479
                121
                             419
                                           61
al Similarity
144; Conserv
                                                                                   100.0%; Score 144; DB 22; ilarity 100.0%; Pred. No. 5.7e-147; Conservative 0; Mismatches 0;
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RESULT
AAE07893
AAE07893;
               AAE07893 standard;
                                  7
                 Protein;
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Modified clostridial heavy chain-superoxide dismutase conjugate 01-NOV-2001 (first entry)

#5

Chimeric - Bacillus stearothermophilus. Chimeric - Influenza virus. Chimeric - Clostridium botulinum. Chimeric - Synthetic. superoxide dismutase; tumour; Neuronal cell; binding domain; translocation domain; stroke; epilepsy; infection; neurodegenerative SOD; botulinum neurotoxin type F; BONT

WO200158936-A2

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RESULT
AAEO7890
ID AAEC
XX
XX
AC AAEC
AC AAEC
XX
DT 01-N
XX
Modi
XX
KW Moun
KW Suppo
KW Suppo
CS Chim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 144;
Chimeric - Bacillus stearothermophilus
                                                                                Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin;
                                                                                                                                                                                                                                                                       01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                      AAE07890;
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07-APR-2000; 2000GB-0008658
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                                                        botulinum neurotoxin type F; BoNT/F.
                                                                                                                                                                                                    Modified clostridial heavy chain-superoxide dismutase conjugate #2.
                                                                                                                                                                                                                                                                                                                                                                                          AAE07890 standard; Protein; 862 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 vgcndtryvgiryfkvfdtelgkteietlysdepdpsilkdfwgnyllynkryyllnllr 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 vfnytqmisisdyinkwifvtitnnrlgnsriyingnlideksisnlgdihvsdnilfki 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tdksitqnsnflningqrgvyqkp 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No. 6
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Modified clostridial heavy chain-superoxide dismutase conjugate #4.
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The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN commain is not a HN commain is not a HN commain of a clostridial neurotoxin and is not a fragment or derivative of CC domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic cubstrances to neuronal cells. They are useful to treat disorders of the CC substances to neuronal cells. They are useful to treat disorders of the CC is including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase (MnSOD), from CC many contained the comprises bacterial Mn-superoxide dismutase (MnSOD), from CC This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from CC specific binding domain from diphtheria neurotoxin and a neuronal cell-specific specific binding domain from botulinum neurotoxin type F (BoNT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells .
01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1999; 99GB-0028530.
07-APR-2000; 2000GB-0008658.
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Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                              AAE07892;
                                                                                    AAE07892 standard; Protein; 887 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Page 40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514643/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shone CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                      121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                              696 tdksitqnsnflningqrgvyqkp 719
                                                                                                                                                                                                                                                                                                                                                                                                                      1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             862 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 144; DB 22; 100.0%; Pred. No. 7.5e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                          Query Match
Best Local S
Matches 144
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Chimeric - I
Chimeric - Chimeric - Chimeric - Chimeric - Chimeric - Chimeric - S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells -
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tumour; infection; neurodegenerative disease; gene thera
superoxide dismutase; SOD; diphtheria neurotoxin; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1999;
07-APR-2000;
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                                                                                                                                                                                                                                                                        Sequence
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                                                              661
                              121
                                                                                                                            601
                                                                                            61
                                                                                                                                                                                                           Local Similarity
                                                                                                                     TDKSITQNSNFLNINQQRGVYQKP 144
                                                         vgcndtryvgiryfkvfdtelgkteietlysdepdpsilkdfwgnyllynkryyllnllr
                                                                        VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                            144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Page 42; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurotoxin type F; BONT/F.
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Corynebacterium diphtheriae.
Clostridium botulinum.
Synthetic.
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2000GB-0008658
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                                                                                                                                                                                                        Score 144; DB 22;
Pred. No. 7.7e-147;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; stroke; epilepsy;
; gene therapy; chimeric;
                                                                                                                                                                                         0;
                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                         887;
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                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuronal cell; binding domain; translocation domain; tumour; infection; neurodegenerative disease; gene tl botulinum neurotoxin type F; BONT/F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 48; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1999;
07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001
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                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translocates
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             121
                                           806
                                                                                                    746
                                                                                                                                                           Watch 100.0%; Score 144; DB 22; Local Similarity 100.0%; Pred. No. 8.9e-147; nes 144; Conservative 0; Mismatches 0;
                                                                       1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             botulinum
                                      TDKSITQNSNFLNINQQRGVYQKP 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutton JM,
                                                                                                                                                                                                                                      1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99GB-0028530.
2000GB-0008658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the therapeutic agent into the neuronal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain with BoNT/F-binding
                                                                                                                                                               Indels
                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stroke;
                                                                                                                                                                                          1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
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RESULT
AAY93309
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                                                                                                                                                                                       Matches 144;
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                       The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93309 standard; protein; 1059 AA.
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 48-51; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A manganese superoxide dismutase (Mn-SOD) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         botulinum neurotoxin serotype F.
                                                                                                                    893
                              121
                                                               833
                                                        11
tdksitqnsnflningqrgvyqkp 916
                TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sutton JM,
                                                                                                                                                                                                                                                                 1059 AA;
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0024282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-GB03699.
                                                                                                                                                                                                  100.0%; Score 144; DB 21; 100.0%; Pred. No. 9.1e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hallis B,
                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silman N;
                                                                                                                                                                                     0;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                Length 1059;
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RESULT 12
AAY93312
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Best Local :
                                                                                                                                                                                                                                                                                                     Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a construct of the invention, comprisin a mitochondrial leader sequence from human managenese superoxide dismutase (Mn-SOD), a Bacillus stearothermophilus Mn-SOD, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as schemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93312 standard; protein; 1084 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 57-60; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200028041-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A manganese superoxide dismutase (Mn-SOD) construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1998;
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                                                  121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 AA;
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0024282.
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                                                                                                                                                                                                                                        100.0%; bred. No. 100.0%; pred. No. 100.0%; pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hallis B, Silman N;
                                                                                                                                                                                                                                                                                                                                  Score 144; DB 21;
Pred. No. 9.3e-147;
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                            Indels
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RESULT 1
AAEO 74000
ID AAEO 74000
XX AAEO
XX AAEO
XX Neux
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KW bott
XX UCO
XX Clos
XX VCO
XX O2-1
PR 07-1
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                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of translocates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shone
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BoNT/F) binding domain used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200158936-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918
                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non toxic polypeptide for delivery of a therapeutic agent atment of a CNS disorder comprising a binding domain that nslocates the therapeutic agent into the neuronal cells -
VENYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vfnytqmisisdyinkwifvtitnnrlgnsriyingnlideksisnlgdihvsdnilfki
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092 AA;
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99GB-0028530
2000GB-0008658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2 translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative in type F; BoNT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50pp; English.
                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                 Score 144; DB 22; Pred. No. 9.4e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain with BoNT/F-binding domain
                                                                                                                                                                                                                                                                                                  Mismatches
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RRESULT 1
AABOTAS
AABOTAS
AABOTAS
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                                                                                                                                                                                                                                            CC The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as Hc) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial toxin. Polypeptides of the invention are CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain which is a hybrid of botulinum neurotoxin type F (BONT/F) and tetanus neurotoxin (TeNT) domain II with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
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                                  Query Match
Best Local
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Chimeric - Clostridium tetani.
Chimeric - Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal cell; binding domain; translocation domain; tumour; infection; neurodegenerative disease; gene tidiphtheria neurotoxin; tetanus neurotoxin; TeNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2000; 2000WO-GB04644.
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                                                                                                                                                           Sequence
                                                                                                                                                                                                                   translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translocates the therapeutic agent into the neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2001
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         Similarity
69; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 46; 50pp;
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2000GB-0008658.
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                                                                                                                                                                                                                         domain
                                                                                                                                                              AA;
                                                                                                                                                                                                                      (BONT/F) and tetanus neurotoxin (TeNT) ain of diphtheria neurotoxin.
                                  47.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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         Score 69; DB; Pred. No. 7.10; Mismatches
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DB 22,
3. 7.1e-66;
0;
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RESULT 15
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ID AAW683
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                                                                                                                                                        This is the amino acid sequence of the histidine-tagged C fragment of Clostridium botulinum (202F strain) type F neurotoxin, encoded by a DNA sequence (see AAV3053) in plasmid pEFHisb. This vector can be used to express BotC soluble C fragment in Escherichia coll host cells, with the recombinant C fragment proteins that an affinity column. The invention relates to recombinant proteins derived from C. botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin cointamination. Preferred hosts for production of recombinant proteins are E. coll, insect cells and yeast cells. The recombinant toxins are used as immunogens for the production of and animals at risk of intoxication with clostridial toxin.
                                                         Overy Match 18.8%; Score 27; DB 19; Best Local Similarity 100.0%; Pred. No. 1.3e-20; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                      Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat humans and other animals at risk of intoxication with clostridial toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antitoxin; vaccine; neurotoxin; toxin F; intoxication; immunogen;
botulism; BotF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium botulinum type F toxin C fragment.
                                                                                                                                  Sequence 448 AA;
                                                                                                                                                                                                                                                                                                                                                                             Example 48; Page 364-365; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV30593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thalley BS, Williams JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum serotype F strain 202F (ATCC 23387).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW68399 standard; Protein; 448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-230234/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OPHI-) OPHIDIAN PHARM INC.
96US-0704159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US15394.
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Search completed: August 15, 2002, 11:12:27
Job time: 319 sec

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
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2: pir2:*
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Match Length DB
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Copyright (c) 1993 - 2000 Compugen Ltd
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RESULT 1 TATURIS RESULT 1 TATURIS RESULT 1 REPORT SPECIES: Clostridium botulinum C; Species: Clostridium botulinum C; Species: Clostridium botulinum C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change C; Accession: 140813; S48108 R; Rest, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Robe R; East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Robe R; East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Robe R; East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Rost R; Reference number: 140644 A; References: Prellminary; translated from GB/EMBL/DDBJ A; Status: prellminary; translated from GB/EMBL/DDBJ A; Cross-references: GB:M92906; NID:g144866; PIDN:AAA23263.1; PII R; Campbell, K.D.; Collins, M.D.; East, A.K. J. Cilin. Microbiol. 31, 2255-2262, 1993 A; Title: Gene probes for identification of the botulinal neurota A; Reference number: 548103; MUID:94013372 A; Accession: S46108 A; Status: prellminary; translation not shown A; Molecule type: DNA A; Cross-references: EMBL:X70816; NID:g407788; PIDN:CAA50147.1; IC; SuperfamIJY. tetanus toxin C; Keywords: neurotoxin.	30 7 4.9 608 31 7 4.9 865 31 7 4.9 814 33 7 4.9 1023 34 7 4.9 1270 36 7 4.9 1276 37 7 4.9 1276 38 7 4.9 1276 38 7 4.9 1276 38 7 4.9 1276 38 7 4.9 1251 40 7 4.9 1251 41 7 4.9 1655 42 30 43 6 4.2 35 44 6 4.2 35
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Clostridium botulinum transparence_revision 16-Aug-1996 #text_chang. s48108 p.T.; Allaway, D.; Collins, M.D.; Rol. 196, 225-230, 1992 the gene encoding type F neurotoxin of Cl 140644 RES> GB:M92906; NID:g144866; PIDN:AAA23263.1; P GB:M92906; NID:g144866; PIDN:AAA23263.1; P S1, 1255-2262, 1993 sfor identification of the botulinal neuro \$48103; MUID:94013372 y; translation not shown A COAND EMBL:X70816; NID:g407788; PIDN:CAA50147.1; the coxin	
_change 16-Jul-1999 .; Roberts, T.A.; Thompson, of Clostridium botulinum1; PID:g144867 neurotoxin gene and specific	phosphogluconate denv polyprotein - phosphatidylinosit hypothetical protein- integrin alpha-9 chypothetical protein - bontoxilysin (EC 3) non-proteollytic bo outer membrane prohypothetical protein protein protein protein protein protein protein protein protein f18014.13 H+-transporting tw H+-transporting tw

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A;Status: nucrec DNA
A;Molecule type: DNA
A;Molecul
         A; Residues: 1-1252 WHE>
A; Cross-references: EMBL: X62683; NID: g40397;
A; Crompbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
                                                                                                                                                                                                                                                                                                                                                                               botulinum neurotoxin type E precursor - Clostridium botulinum (;Speciles: Clostridium botulinum C;Speciles: Clostridium botulinum C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Oct-1999 C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111 R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P. Eur. J. Biochem. 204, 657-667, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain BL6340 C; Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lic C; Superfamily: tetanus toxin C; Keywords: neurotoxin
                                                                                                                                                                                                                                            A;Title: The complete amino A;Reference number: S21178; A;Accession: S21178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;2-422/Product: botulinum neurotoxin type E liq
F;423-1251/Product: botulinum neurotoxin type E
F;412-426/Disulfide bonds: #status predicted
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C;Species: Clostridium butyricum
C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change
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C;Keywords: neurotoxin
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A; Residues: 1-229, 'M', 231-252 <FUJ>
A; Cross-references: EMBL: X53180; NI
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A; Reference number: S16145;
A; Accession: S16145
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R; Poulet, S.; Hauser, D.; Q
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MUID:92174922
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Pred. No.
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2.5e-07;
                                                                                                     PIDN:CAA44558.1;
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e E heavy chain #stat
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                                                                                                          PID:g40398
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                                                A; Nolecule type: DNA
A; Residues: 1-1296 <BIN>
A; Residues: 1-1296 <BIN>
A; Cross-references: GB:M30196; NID:g144864; PIDN:AAA23262.1;
A; Experimental source: strain 62A, subtype A
A; Experimental source: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Clostridium botulinum
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T; Kurazono, H; Wille, M; Frevert, J; Wernars, K; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin A;Reference number: A35294; MUID:90264400
A;Accession: A35294
R;Thompson, D.E.; Brehm, J.K.;
Eur. J. Biochem. 189, 73-81, 11
A;Title: The complete amino ac:
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ISDYINKWIFVTITN ISDYINKWIFVTITN

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T.J.; Shone, C.C.;

Atkinson,

PID: g144865

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A;Experimental source: strain Beluga
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison
A;Reference number: A35294; MUID:90264400
A;Accession: B35294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X70815; NID:g407786; PIDN:CAA50146.1; PID:g407787 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 199: R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R. Biochem. Biophys. Res. Commun. 183, 107-113, 1992
A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C A;Reference number: A60027; MUID:90344918
A;Accession: A60027
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A;Residues: 1-176 'R',178-197,'C',199-339,'R',341-772,'I',774-962,'FE',965-966,'R',96
A;Cross-references: EMBL:X62089; NID:g40393; PIDN:CAA43999.1; PID:g40394
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                                                                                                                                                                F;1-422/Product: botulinum neurotoxin type E light chain *status predicted <LCH> F;423-1252/Product: botulinum neurotoxin type E heavy chain *status predicted <HCH> F;412-426/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                     C; Superfamily: tetanus C; Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain Beluga
A;Note: this fragment was generated by proteolysis with Lys-C rather than with trypsi
C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit
C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-176, 'R', 178-252 <BIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 420-427 < GIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Gimenez, J.A.; DasGupta, 1
Biochimie 72, 213-217, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: JH0256; MUID:92181428
A;Accession: JH0257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 616-982 < CAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                              Query Match
                                                                                                                                                                                                                                                                                                 Superfamily: tetanus toxin
ch 10.4%; similarity 100.0%; 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beluga
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                                  Score 15;
Pred. No.
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                                  DB 2;
2.5e-
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                                                              Length 1252
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A; McJecule type: protein
A; Residues: 867-880;1148-1217,/Y',1219 <GIM>
A; Experimental source: strain Hall
A; Experimental source: strain Hall
A; Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after ex
R; DasGupta, B.R.; Dekleva, M.L.
Blochimie 72, 661-664, 1990
A; Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and arou
A; Reference number: A60025; MUID:91120847
A; Accession: A60025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495
A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                              В
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A;Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate A;Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
C;Reywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot
F;2-444/Product: bontoxilysin A light chain #status experimental <AUTY>
F;243-1296/Product: bontoxilysin A heavy chain #status experimental <AUTY>
F;223,227/Binding site: zinc (His) #status predicted
F;223/Active site: Glu #status predicted
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A;Gene: atx; botA
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A; Residues: 2-6; 445-453, X', 455-457 < CDAS1>
R; DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1987
A; Title: Partial sequence of the light chain of botulinum neurotoxin type A.
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R;Gimenez, J.A.; DasGupta, Ba;
J. Protein Chem. 12, 351-363, 1993
A;Tile: Botulinum type A neurotoxin digested with pepsin yields 132, 97, A;Reference number: A53884; MUID:94000342
A;Accession: A53884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Betley, M.J.; Somers, E.; DasGupta, B.R. Biochem. Biophys. Res. Commun. 162, 1388-1395, 1989 A;Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term A;Reference number: A33401; MUID:89350959 A;Accession: A33401
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A; Residues: 1-12 <FUJ>
A; Cross-references: EMBL:D67030; DDBJ:D50421; NID:g2160224
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A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components A;Reference number: S67988; MUID:96096783
A;Accession: S68220
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A; Accession: S09492
A; Molecule type: DNA
A; Residues: 1,'0',3-26,'V',28-1296 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 2-47 < DAS2>
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A; Accession: A27000
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A; Residues: 1-35 <BET>
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                                              1014 WIFVTITNNRL 1024
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                                                                                                                                                                                                          Similarity
                                                                                                                                                                              Conservative
                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                      7.6%; Score 11; DB 1; 00.0%; Pred. No. 0.004
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                                                                                                                                                                                                          0.0044;
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A;Residues: 1-1296 <RES>
A;Cross-references: EMBL:X73423; NID:g507070; PIDN:CAA51824.1; PID:g507071
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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c;Species: Clostridium botulinum
c;Species: Clostridium botulinum
c;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999
c;Accession: I40645
R;Willems, A.; East, A.K.; Lawson, P.A.; Collins, M.D.
Res. Microbiol. 144, 547-556, 1993
A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type
A;Reference number: I40645
A;Reference number: I40645
A;Recssion: I40645
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-540 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X70821; NID:g407792; PIDN:CAA50152.1; PID:g407793 C;Superfamily: tetanus toxin C;Keywords: neurotoxin
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                                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                  hypothetical protein CC0813 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Apre-2001 **sequence_revision 20-Apr-2001 **text_change 20-Apr-2001 C;Accession: B87350
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A;Tille: Gene probes for identification of the botulinal neurotoxin
A;Reference number: S48103; MUID:94013372
A;Accession: S48110
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C;Species: Clostridium botulinum (fragment)
C;Date: 14-7ul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S48110
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Best Local :
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Best Local Similarity
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5. 0.19;
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A; Molecule type: DNA
A; Residues: 1-1297 <CAM>
A; Cross-references: EMBL: X74162;
C; Superfamily: tetanus toxin
C; Keywords: neurotoxin
                 RESULT
A81295
                                                                                                                                                                                      C;Keywords: calcium binding; EF hand F;14-46/Domain: calmodulin repeat homology <EF1>F;84-116/Domain: calmodulin repeat homology <EF2>
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R; Campbell, K.; Collins, M.D.; East, A.K. Biochim. Biophys. Acta 1216, 487-491, 1993
A; Title: Nucleotide sequence of the gene cc
A; Reference number: S39791; MUID:94092745
A; Accession: S39791
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C;Superfamily: calmodulin; calmodulin repeat homology
                                                                                                                                                                                                                                                                                                                                     myosin regulatory light chain 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992
C;Accession: S20990
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C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
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S39791
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C;Genetics:
A;Gene: CC0813
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A; Residues: 1-156 < ALT>
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 protein Cj1484c [imported] -
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100.0%;
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                                                                                                                                    Score 7;
Pred. No.
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                                                                                                                        Mismatches
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3;
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Campylobacter jejuni (strain
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                                                                                                                                              Length 156;
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myosin regulatory light chain 2 - human N; Alternate names: pre-lymphocyte-specific c; Species: Homo sapiens (man) C; Date: 03-May-1994 #sequence_revision 20-F; C; Accession: S22715 R; Oltz, E.M.; Yancopoulos, G.D.; Morrow, M., EMBO J. 11, 2759-2767, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
S20992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change
C;Accession: A81295
C;Accession: A81295
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher,
C:W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet,
Nature 403, 665-668, 2000
A;Status: not compared with A;Molecule type: mRNA A;Residues: 1-204 <OLT>
                                                A; Reference number: S22715;
A; Accession: S22715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: calmodulin; ca
C; Keywords: calcium binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: S20992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myosin regulatory light chain 2 - mouse C;Species: Mus musculus (house mouse) C;Date: 16-Sep-1992 #sequence_revision C;Accession: S20992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-200 <PAR>
A;Cross-references: GB:ALI39078; GB:ALI11168; NID:96968723;
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The genome sequence of the food-borne A;Reference number: A81250; MUID:20150912 A;Accession: A81295 A;Status: preliminary
                                                                                   A; Title: A novel regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                          F;60-92/Domain: calmodulin repeat homology <EF1>F;130-162/Domain: calmodulin repeat homology <EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S20990
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C; Superfamily:
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A; Residues: 1-202 <ALT>
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Best Local S
Matches 7
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Similarity 100.0%;
7; Conservative (
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                                  conceptual translation
                                                                   MUID:92331628
                                                                                   myosin light chain
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                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No.
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                                                                                                                                                     20-Feb-1995 #text_change
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                                                                                                                    M.A.;
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14;
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                                                                                    distinguishes
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VanVliet, A
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                                                                                                                  G.; Wong, F.;
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Appothetical protein Atu0751 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AI2668
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Wonks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
A;Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; pMID:11743193
A;Recession: AI266
A;Status: prelininary
A;Cross-references: GB1-RE008688; PIDN:AAL41767.1; PID:g17739119; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                       RESULT 15

$28494
dtxA protein - Clostridium difficile

C;Species: Clostridium difficile
C;Species: Clostridium difficile
C;Species: Clostridium difficile
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 15-Oct-1999
C;Accession: JC5344; $28494
C;Accession: JC5344; $28494
R;Braun, V.; Hundsberger, T.; Leukel, P.; Sauerborn, M.; von Eichel-Streiber, C.
Gene 181, J9-38, 1996
A;Title: Definition of the single integration site of the pathogenicity locus in Clostri
A;Reference number: JC5340; MUID:97128764
A;Accession: JC5344
A;Acc
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                                                                                                                                                                                                                     C;Genetics:
A;Gene: dtxA; tcdC
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Best Local Similarity
7; Conserv
Ouery Match 4.9%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches
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nes 7; Conserv
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100.0%; Pred. No. 16;
ative 0; Mismatches
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100.0%; Pred. No. 14;
ative 0; Mismatches
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     0; Indels
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Qy 83 KTEIETL 89
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Db 70 KTEIETL 76
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Search completed: August 15, 2002, 11:14:07 Job time: 259 sec

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Title:
Perfect score:
Sequence:
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No.
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SUBSTRATE. pubMed=8175689; pubMed=8175689; sister A., Binz T., sis	-//(19 ROM N. ed=840 , Coll ificat ificat n of n	ROM N.A. PubMed-7764998; M.D.; M.D.; M.D.; M.D. genes encoding of the sequence of in nonproteolytic Clored.	PubMed-1398040; Ison P.T., Allaway Ipson D.E.; ene encoding type itt. 75:225-230(199	Bacillus/Clos	Created) Last sequence Last annotation	ARD; PRT;	ALIGN	114 1 Y211_BUCAI 128 1 WNT8_EVATR 137 1 IPPD_PIG 148 1 AZUR_METFL 151 1 YG98_CLOAB 163 1 YATPX_OCHNE 167 1 YXL_BACSU 181 1 GLG2_HORVU 181 1 RERB_ARATH 195 1 RERB_ARATH 195 1 RERB_ARATH 195 1 RERB_ARATH
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                                                                        MEDLINE-92181428; PubMed=1543481; Populet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; Poquences of the botulinal neurotoxin E derived from Cl botulinum type E (strain Beluga) and Clostridium butyric ATCC 43181 and ATCC 43755).";
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01-MAR-2002 (Rel. 41, Last annotation
Botulinum neurotoxin type E precursor
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PRINTS; PR00760; BONTOXILYSIN; 1.
Probom; PD001963; BontoXilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR000395;
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MISCELLANEOUS: THERE ARE SEVEN B, Cl, D, E, F
BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, F
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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SUBUNIT: DISULFIDE-LINNED HETERODIMER OF A LIGHT CHAIN (L) AND A
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
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sen the Swiss Institute of Bioinformatics and the EM
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                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=94063091; PubMed=8243675;

Schlavo G., Santtuci A., Dasgupta B.R., Mehta P.P.,

Benfenati F., Wilson M.C., Montecucco C.;
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Biochimie 72:213-217(1990).
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MEDLINE-85197963; PubMed-3888113;
Schmidt J. J., Sathyamoorthy V., Dasgupta B.
"Partial amino acid sequences of botulinum
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"Botulinum neurotoxin type F
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SUBCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS
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FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 180-ARG-[-ILE-ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 180-ARG-[-ILE-ENDOPERTICALYZES]
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T., Kurazono H., Wille M., Freve;
complete sequence of botulinum no
other clostridial neurotoxins.";
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X62089; CAA43999.1;
X62683; CAA44558.1;
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ACT_SITE
                                     MEDLINE=91237316; PubMed=2033376; FUjii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; "Cloning of a DNA fragment encoding the 5'-terminus of the type E toxin gene from Clostridium butyricum strain BL6340. J. Gen. Microbiol. 137:519-525(1991).
                               type E toxi. J. Gen. Microbiol.
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STRAIN-ARCC 43181, AND ARCC 43755;
MEDLINE-92181428; pubmed-s1543481;
MEDLINE-92181428; pubmed-s1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium buturicum (strain Botulinum type E (strain Beluga) and Clostridium butyricum (strain ARCC 43181 and ARCC 43755).";
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Clostridium butyricum.
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Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
  SEQUENCE OF 1-48
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BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
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O1-JUL-1993 (Rel. 26, Last sequence update)
O1-MR-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
(BONTOXILYSIN A) (BOTOX) [Contains: Botulinum neurotoxin A, light-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions will use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNIT: DISULFIDE LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.
-!- SUBCELLAUROUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULTHUM NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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"Neurotoxin type E from Clostridium botulinum and C. butyricum;

partial sequence and comparison.";

PASSEB J. 2:A1750-A1750(1988).

-!- EUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEED POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01142; Peptidase_M27; 1.
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Gimenez J.,
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PROSITE; PS00142; ZINC_PROTEASE; 1
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PIR; S16145; S16145.
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BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
K -> M (IN REF. 2).
5 MW; 8171B5B2C2312857 CRC64;
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Botulinum

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MEDLINE-97016817; PubMed-8863443;
East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89350959; PubMed=2669749;
Betley M.J., Somers E., Dasgupta B.R.;
"Characterization of botulinum type A neurotoxin gene:
the N-terminal encoding region ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>3</u>.
           SEQUENCE OF 448-464 AND 872-895.
MEDLINE=89024662; PubMed=3178218;
                                                                                                                                                                                                                          Schmidt J.J., Sartymoorthy V., Dasgupta B. "Partial amino acid sequence of the heavy
                                                                                                                                                                                                                                                     SEQUENCE OF 1-16. MEDLINE=84178501; PubMed=6370252;
                                                                                                                                                                                                                                                                                          components
FEBS Lett.
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MEDLINE=90235864;
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Dasgupta B.R., Foley J., Niece R
"Partial sequence of the light c
Biochemistry 26:4162-4162(1987).
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MEDLINE-96096783; PubMed-8521962;
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                                               "Botulinum neurotoxin type A: sequence N-terminus and around the nicking site Biochimie 72:661-664(1990).
                                                                                       Dasgupta
                                                                                                 MEDLINE-91120847;
                                                                                                                                                                                                                                                                                                                 Fujita R., Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.;
"Molecular characterization of two forms of nontoxic-nonhemagglutinin
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                                                                                                                                                                                                                 botulinum neurotoxin type A.";
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                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal encoding
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C., Atkinson T., Melling J., Minton N.P.;
plete amino acid sequence of the Clostridium botulinum type
in, deduced by nucleotide sequence analysis of the encoding
                                                                                       B.R., Dekleva M.L.
                                                                                                                 OF 1-5
                                                                                                                                                                                                     Biophys.
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                                                                                                                                                                                                                                                                                          of Clostridium botulinum type A progenitor toxins."; 376:41-44(1995).
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 Dasgupta
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B.R.,
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Shone C.C., Hambleton P., Melling J.;
"Inactivation of Clostridium btulinum type A neurotoxin and purification of two tryptic fragments. Proteolytic ac the COOH-terminus of the heavy subunit destroys toxin-bin activity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem.
                                                                                                          the treatment of strabismus and blepharospasm associated dystonia and cervical dystonia. Also used for the treatment for the treatment and spasm and a number of other neurological disor characterized by abnormal muscle contraction. MISCELLANDOUS: There are seven antigenically distinct for botulinum neurotoxin: Types A, B, Cl. D, E, F, and G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-cln-l-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted. PHARMACEUTICAL: Available under
                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Limited hydrolysis of pronouncexocytosis apparatus, synapcobravins, sed detected action on small molecule substrates, SUBUNIT: Disulfide-linked heterodimer of a limited process.
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                                                                                                                                                                                                                                                        heavy chain
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R., Niemann
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Pubmed=9783750;
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Yamasaki S., B
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BXA2_CLOBO STANDARD;
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Q45894; P77780;
Q1.MAR-2002 (Rel. 41, Created)
Q1.MAR-2002 (Rel. 41, Last sequence update)
Q1.MAR-2002 (Rel. 41, Last annotation update)
B0.Tullnum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
B0.Tullnum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
B0.Tullnum neurotoxin A, light-
MEDLINE-94143603; PubMed-8310180; Willems A., East A.K., Lawson P.A., Collins M.D.; Willems A. East A.K., Lawson P.A., Collins M.D.; "Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison with
                                                                                                                     Clostridium botulinum.
                                                                                                                                Chain; Botulinum ne
BOTA OR BNA OR ATX.
                                                                                                                                                                                                                                                                                    1013 WIFVTITNURL 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000395; Bontoxilysin.
InterPro: IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52066; CAA36289.1; -.
EMBL; M30196; AAA23262.1; -.
EMBL; X92973; CAA63551.1; -.
EMBL; D67030; BAA11051.1; -.
EMBL; M27892; AAA23269.1; -.
                                                           SEQUENCE FROM N.A.
                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M27.002; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                 NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmaceutical;
                                                                                                                                                                                                                                                                                                  17 WIFVTITNNRL 27
                                                                                                                                                                                                                                                                                                                               A35294; BTCLAB.
S09492; S09492.
BTA; 01-OCT-99
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1234
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365
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                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                              149322
                                                                                                                                                                                                                                                                                                                                                           7.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                           F->A: DECREASE IN ENZYMATIC ACTIVITY.
Y->A: DECREASE IN ENZYMATIC ACTIVITY.
P-> Q (IN REF. 1).
E-> P (IN REF. 9).
T-> L (IN REF. 8).
S-> K (IN REF. 8).
S-> K (IN REF. 8).
                                                                                                                                                                                                                                                                                                                                              Score 11;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E->A: DRASTIC DECREASE IN ENZYMATIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
V -> A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOTULINUM NEUROTOXIN A, LIGHT-CHAIN. BOTULINUM NEUROTOXIN A, HEAVY-CHAIN. ZINC (CATALYTIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CATALYTIC).
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3. 0.0021;
0;
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                                                                              Query Match
Best Local
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                                                                                                                             TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                   DISULFID
                                                                                                                                                                                                               CHAIN
METAL
                                                                                                                                                                                                                                                                                                                                            EMBL; X73423; CAA51824.1; -. EMBL; X87974; CAA61234.1; -. HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
[2]
[2]
SEQUENCE OF 1-65 FROM N.A.
                        1013 WIFVTITNNRL 1023
                                                                                                                                                                                          METAL
                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                             Neurotoxin;
                                                                                                                                                                                                                                                                        PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                          Pfam; PF01742; Peptidase_M27;
                                                                                                                                                                                                                                                                                                                                  MEROPS; M27.002;
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                                               17 WIFVTITNNRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy cha
                                                                     1 Similarity
11; Conserv
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                                                                      Conservative
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1295
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675
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                                                                     Score 11; DB; Pred. No. 0.0
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Query Match Best Local Matches

CONFLICT CONFLICT CONFLICT

MUTAGEN MUTAGEN

MUTAGEN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      failure (By similarity).

-I- CANALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.
-I- SUBUNIT: Disuffide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-[-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Hydrolase; Metalloprotease; Zinc.
                                                                                                                                                                                                                                                                          ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
INC (CATALYTIC) (BY SIMILARITY).
BY CIVIL ABOTUL
                                                                                                                                                                        5DA04A13D98D6372 CRC64;
DB 1; Len. 0.0021;
                                                                  Length 1295;
           Indels
       0;
           Gaps
       0;
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RESULT
BXG_CLC
                         Query Match
Best Local :
Matches
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Q60393;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLOBO
                                                                                                                       DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with other clostridial neurotoxins.";
Biochim. Biophys. Acta 1216:487-491(1993).
Biochim. Biophys. Acta 1216:487-491(1993).
-i- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNAL AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campbell K., Collins M.D., East A.K.; "Nucleotide sequence of the gene coding for C: (Clostridium argentinense) type G neurotoxin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Create 01-NOV-1997 (Rel. 35, Last s 01-MAR-2002 (Rel. 41, Last a Botulinum neurotoxin type G
                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X74162; CAA52275.1;
HSSP; P10845; 3BTA.
MEROPS; M27.002; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                        Prodom; PD001963; Bontoxilysin; 1. PROSITE; PS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                          METAL
                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                      Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94092745; PubMed=8268233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1491;
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                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntax detected action on small molecule substrates.

SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L), HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTUMILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNERORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELIULAR LOCATION: Secreted (By similarity).
MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT
BOTULINUM NEUROPOXIN: TYPES A, B, C1, D, E, F, AND G.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                           PF01742; Peptidase_M27; S; PR00760; BONTOXILYSIN.
  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes;
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  Conservative
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                                                                                                                                                                     441
1296
229
230
233
                         5.6%;
100.0%;
                                                                                                                  metalloprotease; Zinc.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BOTULINUM NEUROTOXIN G
BOTULINUM NEUROTOXIN G
SINC (CATALYTIC) (BY S:
BY SIMILARITY.

                                                                                                                       149013
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Last annotation update)
type G precursor (EC 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Clostridium
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                         Score 8;
Pred. No.
  Mismatches
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8;
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                                                                                                                                                                     (BY SIMILARITY).
                                                Length 1296
                                                                                                                                                                                                                     N G, LIGHT-CHAIN.
N G, HEAVY-CHAIN.
Y SIMILARITY).
                                                                                                                     CRC64;
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E SPINAL CORD
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Best Local
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P76554;
30-MAY-2000
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-917426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Ro
                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Cre
30-MAY-2000 (Rel. 39, Las
16-OCT-2001 (Rel. 40, Las
Ethanolamine utilization
                                                                                                                                                                                                                                                                                                                                                                                                                 _ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antioxidant; Complete proteome.
ACT_SITE 40 40 BY
SEQUENCE 199 AA; 22581 MW;
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16-OCT-2001
                                                                                                                                                                                                                                                Ethanolamine
EUTT OR B2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 407:508-513(2000).
-!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kuepp A., Graml W., Santos-Martinez M.-L., Koretke K.K.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumed
"The genome sequence of the thermoacidophilic scavenger
acidophilum.";
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                                                                                                                                                                                                                     Escherichia coli.
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Pfam; PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-DSM 1728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea;
                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                             Escherichia
                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL445066; CAC12083.1; -.
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16-OCT-2001
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40, Last sequence up
40, Last annotation
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Pred. No.
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4E266162F5D58162 CRC64;
                                                                                                                                                                                                   subdivision;
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         T., Burland
Mayhew G.F
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EC
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us-08-981-087a-3.rsp

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Best Local
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R., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                 Kofold E.C., Rappleye C.A., Stojiljkovic I., Roth J.R.; "The 17-gene ethanolamine (eut) operon of Salmonella typhimurium encodes five homologues of carboysome shell proteins."; J. Bacteriol. 181:5317-5329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTT_SALTY STANDARD; PRT; 267 AA.

9ZEFV4;

09ZEFV4;

10-MAY-2000 (Rel. 39, Created)

10-MAY-2000 (Rel. 39, Last sequence update)

10-MAR-2002 (Rel. 41, Last annotation update)

11-MAR-2002 (Rel. 41, Last annotation update)

12-MAR-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000332; AAC75512.1; -. ECOGene; EG14189; eutT.
Transferase; Complete proteome.
SEQUENCE 267 AA; 30171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - PUNCTION: CONVERTS CON12 TO ADOB12 (BY SIMILARITY).
- CATALYTIC ACTIVITY: ATP + cob(I)alamin + H(2)O = phosphate diphosphate + adenosylobalamin.
- PATHWAY: ETHANOLAMINE UTILIZATION.
                                                               -!- FUNCTION: CONVERTS CNB12 TO ADOB12 (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + cob(I)alamin + H(2)O = phosphate diphosphate + adenosylobalamin.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-LT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                    Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99395039; PubMed=10464203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                               "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=602;
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o. 7.4;
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RESULT 10

VALI_CLVK

ID VALI_CLVK STANDARD; PRT

ID VALI_CLVK STANDARD; PRT

AC P14982;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequen

DT 01-JUN-1994 (Rel. 29, Last annota

DE ALI protein (40.4 kDa protein).
    RESULT 11
VAL1_CLVN
ID VAL1_C
AC P14972
DT 01-APF
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Best Local
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Probom
VAL1_CLVN
P14972;
01-APR-1990
01-APR-1990
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InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1 1.
PRINTS; PR00227; GEMCOATAL1.
ProDom; PD000736; Gemini_AL1; 1.
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"Nucleotide sequence of cassava latent virus DNA.";
Nature 301.260-262 (1983).
-i-. SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cassava latent virus (strain West Kenyan Viruses; ssDNA viruses; Geminiviridae; Be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                     68 TITNNRL 74
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40346 MW;
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100.0%; Pr
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Pred. No.
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o. 9.7;
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RESULT
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Best Local
                                            STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                             Q60281;
01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                               _METJA
  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90174930; PubMed-2308831; Morris B., Coates L., Lowe S., Richardson K., Eddy P.; "Nucleotide sequence of the infectious cloned DNA comp African cassava mosaic virus (Nigerian strain)."; Nucleic Acids Res. 18:197-198(1990).
                                                                                                                                                                                                                                                                                     Hypothetical MJECL21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X17095; CAA34953.1; -.
PIR; S07594; S07594.
InterPro; IPR001191; Gemini_AL1.
Pfam; PF00799; Gemini_AL1; 1.
PRINTS; PR00227; GEMCOATAL1.
PRINTS; PR00227; GEMCOATAL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00227; G
ProDom; PD000736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cassava latent virus (strain Nigerian)
Viruses; ssDNA viruses; Geminiviridae;
                                        jannaschii
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              Methanococcus
                                                                                                                                                                                                                                                         Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                       Methanococcus jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC1
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AL1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITNNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
 SWISS-PROT entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                         273:1058-1073(1996).
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(Rel.
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(40.4
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                                                                                                                                                                                                                                                                                               protein MJECL21.
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kDa
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40435
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 is
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                                                                                                                                                                                                                                                        Methanococcales; Methanococcaceae;
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copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₩,
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3; Pred. No. 9.7
0; Mismatches
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; 1DB16BB0CB2D5E2C CRC64;
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. 9.7;
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produced
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through
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 collaboration
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Query Match Best Local S Matches 7

Similarity 7; Conserv

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

4.9%; Score 7; 1 100.0%; Pred. No.

DB 13;

Length 508

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
Hypothetical
TRANSMEM
SEQUENCE 50
                                                                                                                                                                                                                                                             Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Cerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zh. Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical AF2205.
                                                          EMBL; AE000953; AAB89056.1; -.
                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-VC-16 / DSM 4304 / ATCC 49558; MEDLINE-98049343; PubMed-9389475;
                                              TIGR; AF2205;
                                                                                                                                                                                                                                                       Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            028078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L77118; AAC37092.1; -. TIGR; MJECL21; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
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   508
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                             protein;
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   AA;
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   56562 MW;
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100.0%; Pr
0;
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                              Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 1; Pred. No. 11; 0; Mismatches
                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome.
DBADF2C5C43A4F90 CRC64;
   85823142F601FC6D CRC64;
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                             Complete
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                                                                                                                    Usage
                              proteome
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유양

373 ITNNRLG

28 379

22 ITNNRLG

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RESULT EDD_HEI ID EI AC PI DT 0: DT 10 DT 10 DE PI DE GN EI GN He
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Best Local
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                                                                                                                                                                 HELPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate = 2-dehydro-3-deoxy-6-phospho-D-gluconate + H(2)O.
-!- phospho-D-gluconate + H(2)O.
-!- PATHWAY: KEY ENZYME IN THE ENTNER-DOUDOROFF PATHWAY.
-!- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Urila-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDD_HELPU STANDARD; PRT; 608 AA.

Q9ZKB3;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Phosphogluconate dehydratase (EC 4.2.1.12) (6-phosphogluconate
                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Phosphogluconate dehydratase (EC 4.2.1.12) (6-phosphogluconate
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001530; AAD06597.1; -.
InterPro; IPR000581; ILVD_EDD.
Pfam; PF00920; ILVD_EDD; 1.
ProDom; PD002691; ILVD_EDD; 1.
PROSITE; PS00886; ILVD_EDD_1; 1.
PROSITE; PS00887; ILVD_EDD_2; 1.
LVASS: COMPILE DED_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
Helicobacter pylori (Campylobacter pylori).
                      EDD OR HP1100
                                        dehydratase)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDD OR JHP1026.
                                                                                                                                                                                                                               276 LIDEKSI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                    38 LIDEKSI 44
                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome CE 608 AA; 6660:
                                                                                                                                                                                                                                                                                                      7; Conserv
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        66603 MW; 978A046F3AE15F98 CRC64;
                                                                                                                                                                                                                                                                                                4.9%; Score 7; DB 1 100.0%; Pred. No. 16; tive 0; Mismatches
                                                                                                                                           PRT;
                                                                                                                                           608 AA.
                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                   Length 608;
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В
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                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                InterPro; IPRO00581; ILVD_EDD.
Pfam; PF00920; ILVD_EDD; 1.
ProDom; PD002691; ILVD_EDD; 1.
PROSITE; PS00886; ILVD_EDD_1; 1.
PROSITE; PS00887; ILVD_EDD_2; 1.
Lyase; Complete proteome.
SEQUENCE 608 AA; 66655 MW; 47E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-26695 AFICC 700392;
MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Klark H.-P., Gill S., Dougherty B.A.,
Pleischmann R.D., Ketchum K.A., Klark H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., GGoayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000616; AAD08143.1; -. TIGR; HP1100; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                      276 LIDEKSI 282
                                                                                                                        38 LIDEKSI 44
                                                                                                                                                           Local Similarity les 7; Conserv
                                                                                                                                                           Conservative
                                                                                                                                                                           4.9%;
                                                                                                                                                                                                                                                  66655 MW; 47EF7E62E3371F59 CRC64;
                                                                                                                                                                           Score 7;
; Pred. No
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A_Geneseq_032802:*

1: SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

2: SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS	ABB61650	ABB71869	ABG00708	ABB64387	ABB65142	ABB64051	AAY90687	AAY90682	AAW93889	ABB67658	AAU35171	AAU33386	AAY42169	AAW93890	AAY24976	AAW46873	ABB63292	AAW68395	AAR23652	AAR12576	AAY95073	AAG82013	AAY20026	AAY20027	AAE10807	AA006221	AAB69310	AAW68396	AAB04094	AAY77137	4	₹	713	AAE07900
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Novel polypeptides (AAW09014-17) respectively comprise amino acids	Claim 5; Page 19; 37pp; English.	recombinant vaccine prodn.	munogenic type F botulinum toxin polypeptide(s) - allows	WPI; 1997-065467/06.	Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA;	(MICR-) MICROBIOLOGICAL RES AUTHORITY.	12-JUN-1995; 95GB-0011909.	12-JUN-1996; 96WO-GB01409.	27-DEC-1996.	WO9641881-A1.	;	Clostridium botulinum type F strain Langeland.	Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism.		Immunogenic type F botulinum toxin polypeptide (aall36-1278).	31-MAR-1997 (first entry)		AAW09017;		AAW09017 standard; Protein; 143 AA.	7 1

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RESULT AAWO9014
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Best Local
                         A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278) of a type F botulinum neurotoxin (BoNT/F), and can be produced using a synthetic gene (AAF48101) based on the natural gene sequence (AAF48101) for the heavy chain. The polypeptides its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin, making the useful for vaccine prodn. Recombinant polypeptides can be
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       produced
                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                 Immunogenic type F botulinum toxin polypeptide(s) recombinant vaccine prodn.
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DB; AAT48100.
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Pred. No. 5.7e-140;
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12-MAY-1999;
12-MAY-1999;
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12-MAY-1999;
12-MAY-1999;
                                                               Claim 3;
                                                                              New nucleic acids encoding the the heavy chain of botulinum vaccine against botulism
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                                       chain and then posttranslationally nicked,
                                               Botulism neurotoxins are translated as a
                                                                                                                                                                                                                                                                                         Clostridium
                                                                                                                                                                                                                                                                                                                                                Botulism
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                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                              RKNTSSNGCFWSFISKEHGWQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-016048/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nifsntrlytgveviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maltose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                      rkntssngcfwsfiskehgwqen
                                                                                                                                          LA,
                                                                                                                 AAA54490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                               Fig 9b;
                                                                                                                                                                                                                                                                                                                                               toxin heavy
                                                                                                                                                         ARMY MEDICAL
                                                                                                                                        Byrne
                                                                                                                                                                                                                                                                                         botulinum
                                                                                                                                                                                                                                                                                                                        vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                          2000WO-US12890
                                                                                                                                                                                                99US-0133865.
99US-0133866.
99US-0133867.
99US-0133868.
                                                                                                                                                                                 99US-0133869
99US-0133873
                                                                                                                                                                          99US-0146192
                                                                                                                                          MP,
                                                               73pp; English.
                                                                                                                                                                                                                                                                                                                                 neurotoxin;
                                                                                                                                                                                                                                                                                                                        antigen;
                                                                                                                                                                                                                                                                                                                                               chain C-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                          Middlebrook
                                                                                                                                                         RES & MATERIAL
                                                                                                the carboxy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
                                                                                         neurotoxin
                                                                                                                                                                                                                                                                                                                        heavy chain;
immune respon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143; DB 18; Pred. No. 1.5e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             facilitate purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                        JL,
                                                                                                                                                                                                                                                                                                                        response;
                                                                                                                                                          COMMAND
                                                                                                                                          Lapenotiere
                                                                                         ರ್ಣ ಜ
                                               single 150 kDa
                                                                                                                                                                                                                                                                                                                                 recombinant
                                                                                       amino-terminal serotype A-G, u
                                        forming a
                                                                                                                                                                                                                                                                                                                         vaccine;
                                                                                                                                                                                                                                                                                                                                               (serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                          Ξ
                                        dichain
                                                                                                                                                                                                                                                                                                                                expression;
                                                                                                                                                                                                                                                                                                                         bacterium;
                                               polypeptide
                                                                                         l portions useful as
                                                                                                                                                                                                                                                                                                                                                 F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                 of
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consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BONT) can be used in recombinant

expression

expressed

in

transformed

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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Disclosure; Fig 18b; 73pp; English
                                                                                                                                                                                                                                                                 12-MAY-2000; 2000WO-US12890
                                                                                                                                                                                                                                                                                          16-NOV-2000.
                                                                                                                                                                                                                                                                                                                 WO200067700-A2
                                                                                                                                                                                                                                                                                                                                          Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                        Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                             Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB04103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB04103 standard; Protein; 432 AA
                          New nucleic acids encoding the carboxy-
the heavy chain of botulinum neurotoxin
vaccine against botulism
                                                                                                                Smith LA,
                                                                                                                                                                              12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                          12-MAY-1999;
                                                                                                                                       (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                 12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 rkntssngcfwsfiskehgwgen 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                           2001-016048/02.
DB; AAA54499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 AA;
                                                                                                              Byrne MP, Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                          99US-0133865.
99US-0133866.
99US-0133867.
99US-0133869.
99US-0133873.
                                                                                                                                                                99US-0146192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 143; DB 22; 100.0%; Pred. No. 1.5e-139; tive 0; Mismatches 0;
                                                                                                              Lapenotiere
                                     or amino-terminal portions of of serotype A-G, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE07894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin producting bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                    Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 432 AA;
                                                                                                                                                                                02-DEC-1999; 99GB-0028530.
07-APR-2000; 2000GB-0008658.
                                                                                                                                                                                                                                                                                                                                               Chimeric - Corynebacterium diphtheriae. Chimeric - Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE07894 standard; Protein; 645 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botulism neurotoxins are translated as a single 150 kDa polypeptide
                   New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that
                                                                                                                                                                                                                                       04-DEC-2000; 2000WO-GB04644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001 (first entry)
translocates the therapeutic agent into the neuronal
                                                                        WPI; 2001-514643/56.
                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                           16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 rkntssngcfwsfiskehgwqen 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 nifsntrlytgveviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpe 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ر
ت
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                            Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 143; DB 22; 100.0%; Pred. No. 1.5e-139;
                                                                                                            Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the
                                                                                                                                                                                                                                  Chimeric - Bacillus stearothermog
Chimeric - Influenza virus.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
WPI; 2001-514643/56
                                                                                            02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
                                                                                                                                                                                                                                                                                                                    Neuronal cell; binding domain; translocation domain; stroke; eptumour; infection; neurodegenerative disease; gene therapy; chi superoxide dismutase; SOD; botulinum neurotoxin type F; BONT/F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain of botulinum neurotoxin type F
                               Shone CC,
                                                                                                                                            04-DEC-2000; 2000WO-GB04644
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE07893 standard; Protein;
                                                                                                                                                                            16-AUG-2001.
                                                                                                                                                                                                          WO200158936-A2.
                                                                                                                                                                                                                                                                                                                                                                                    Modified clostridial heavy chain-superoxide dismutase conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                            (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BoNT/F) with translocation domain of diphtheria neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nifsntrlytgveviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kiiklirtsnsnnslgqiivmdsignnctmnfqnnnggnigllgfhsnnlvasswyynni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                               Sutton JM,
                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                               Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 143; DB 22;
Pred. No. 2.2e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                      chimeric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                     #
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Best Local Sir Matches 143; Query Match Best Local

Similarity

100.0%;

Score 143; DB 22; Pred. No. 2.3e-139; Mismatches

Length Indels

685; 0,

Conservative

0;

0,

Gaps

0

Sequence

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CC therapeutic agent to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated CC as Hc) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain (amino CC domain of HC, designated as HN), that translocation domain is not a fragment into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn superoxide dismutase (MnSOD), from CC conjugate comprises bacterial Mn superoxide dismutase (MnSOD), from CC conjugate comprises bacterial Mn superoxide dismutase (MnSOD), from CC binding domain from botulinum neurotoxin type F (BoNT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 43; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocates the therapeutic agent into the neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for the
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RESULT
AAE07890
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Chimeric - Corynebacte
Chimeric - Clostridium
Chimeric - Synthetic.
02-DEC-1999;
                                                                         04-DEC-2000; 2000WO-GB04644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour; infection; neurodegenerative disease;
superoxide dismutase; SOD; diphtheria neurotox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum neurotoxin type F;
                                                                                                                                                       16-AUG-2001
                                                                                                                                                                                                                                    WO200158936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified clostridial heavy chain-superoxide dismutase conjugate
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                                                                                                                                                                                                                                                                                                                                                   Corynebacterium diphtheriae Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus
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    99GB-0028530
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gene therapy; chimeric;
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CC This conjugate comprises bacterial Mn superoxide dismutase (MnSOD), from CC Encillus stearothermophilus, linker that can be cleaved by factor Xa, CC translocation domain from diphtheria neurotoxin and a neuronal cell-sxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 143;
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Best Local
Chimeric - Homo sapiens.
Chimeric - Bacillus stearothermophilus.
Chimeric - Corynebacterium diphtheriae.
Chimeric - Clostridium botulinum.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                      Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                 botulinum neurotoxin type F; BoNT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified clostridial heavy chain-superoxide dismutase conjugate #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain of a clostridial neurocoxin and is not a fragment or derivative of a NN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful to treat disorders of the substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the substances to neuronal cells. They are useful to treat disorders to the constructs and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises a mitochondrial leader sequence from human Mn-superoxide dismutase (MnSOD), MnSOD from Bacillus stearothermophilus, linker that can be cleaved by thrombin, translocation domain from diphtheria neurotoxin and a neuronal cell-specific binding domain from obtulinum neurotoxin type F (BONT/F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as Hc) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as Hy), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN
                                      C. botulinum C2 translocation domain with BoNT/F-binding domain #2.
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07-APR-2000; 2000GB-0008658
Neuronal cell; binding domain; translocation domain; stroke; epilepsy,
                                                                            01-NOV-2001
                                                                                                                  AAE07901;
                                                                                                                                                      AAE07901 standard; Protein; 1032 AA
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                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                      kiiklirtsnsnnslgqiivmdsignnctmnfqnnnggnigllgfhsnnlvasswyynni 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   887 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 143; DB 2:
Pred. No. 3e-139
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RESULT 1
AAY93309
ID AAYS
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                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a non toxic polypeptide, for delivery of a CC therapeutic agent to a neuronal cell, which comprises a binding domain CC (carboxy terminal half of heavy chain (HC) off a neurotoxin, designated CC as HC) that binds to the neuronal cell and a translocation domain (amino CC terminal half of HC, designated as HN), that translocation domain is not a HN CC domain of a clostridial neurotoxin and is not a fragment or derivative of CC a HN domain of a clostridial neurotoxin and is not a fragment or derivative of CC useful for the treatment of a disease state associated with neuronal CC cells. The polypeptide constructs are useful for delivering therapeutic CC substances to neuronal cells. They are useful to treat disorders of the CC useful infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum CC neurotoxin type F (BoNT/F) binding domain used in the exemplification of the invention of
                                                                                                                                                                                                                                                                                                                                                     Matches
             A manganese
                                          04-SEP-2000
                                                                                                                                                                           1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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07-APR-2000;
                                                                       AAY93309
                                                                                                AAY93309 standard; protein; 1059
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                                                                                                                                                                                                                                    950
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                            990
                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100. nes 143; Conservative
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                                                                                                                                                                                                                                                                                                         1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                              RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                        nifsntrlytgveviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpe 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-514643/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; neurodegenerative disease;
um neurotoxin type F; BONT/F.
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                                                                                                                                                                                                                                                                                                                                                                                                                          1032 AA;
             superoxide
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                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                              100.0%;
             dismutase
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                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                 Score 143; DB 22;
Pred. No. 3.4e-139;
); Mismatches 0;
                                                                                                    A
             (Mn-SOD)
             construct
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                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                Gaps
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Query Match
Best Local S
Matches 143
                                                                                                                                                                                                                                                                    by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Bacillus stearothermop
Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell neuronal cell targeting component; NCTC; neuronal disease; notidative stress; ischemic stroke; trauma; Parkinson's dismutilation's disease; motor neurone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful delivering superoxide dismutase to neuronal cells to treat iscl
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                            Local Similarity
                               Н
NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-376553/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sutton JM,
                                                                                                                                                                                                                            1059 AA;
                                                                                100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 48-51; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0024282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hallis B,
                                                                                     0,
                                                                             Score 143; DB 21;
Pred. No. 3.5e-139;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silman
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                                                                                     Indels
                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treat ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell;
                                                                                                                                            1059;
                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising
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                                                                                  Gaps
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RESULT 11
AAY93312
                       04-SEP-2000
                                                                AAY93312 standard;
                                                                                                                        1037
                                            AAY93312;
                                                                                                                                             121
                                                                                                                                                                     977
                                                                                                                                                                                                               917 nifsntrlytgveviirkngstdisntdnfvrkndlayinvvdrdveyrlyadisiakpe 976
                                                                                                                                                                                          61
                                                                                                                                   RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                   rkntssngcfwsfiskehgwqen
superoxide
                     (first entry)
                                                                 protein; 1084
 dismutase
                                                                  A
 (Mn-SOD)
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RESULT 1
AAE07900
ID AAEC
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AC AAEC
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DT 01-N
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01-NOV-2001
                                                                                                                                                                                                                                                         1062 rkntssngcfwsfiskehgwgen 1084
                                                                                                                                                                                                                                                                                                                                                                    1002 kiiklirtsnsnnslgqiivmdsignnctmnfqnnnggnigllgfhsnnlvasswyynni 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manganese superoxide dismutase; Mm-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease;
                                                                                                               AAE07900 standard; Protein; 1092 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 57-60; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376553/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998;
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                                                            AAE07900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                motor neurone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                   61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1084 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 143; DB 21;
Pred. No. 3.6e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1084;
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RESULT 13
AAY77138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a non toxic polypeptide, for delivery of a characteristic agent to a neuronal cell, which comprises a binding domain coarboxy terminal half of heavy chain (HC) of a neurotoxin, designated cas HO) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic coagent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic coals. The polypeptide constructs are useful to treat disorders of the country of the country of the polypeptide constructs are useful to treat disorders of the country of the present sequence is C. Sottlinum C2 enterotoxin translocation domain with botulinum cas enterotoxin translocation domain with botulinum of the invention.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 143; Conserv
AAY77138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells - \,
                                    AAY77138 standard; Protein; 432 AA
                                                                                                                                 1070 rkntssngcfwsfiskehgwgen 1092
                                                                                                                                                                                                             1010 kiiklirtsnsnnslgqiivmdsignnctmnfqnnnggnigllgfhsnnlvasswyynni 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999; 99GB-0028530
07-APR-2000; 2000GB-0008658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. botulinum C2 translocation domain with BoNT/F-binding domain #1.
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 47; 50pp; English.
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                                                                                                                                                        121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                 61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1092 AA;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 143; DB 22; 100.0%; Pred. No. 3.6e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 1092;
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                                                                                                                                                                                                                                                                                                                   a Venezuelan equine encephalitis virus (VEE) replicon vector. Use of this vector results in the production of large amounts of a protein cencoded by a sequence cloned into the replicon. The constructs are used to produce vaccines against botulism. The proteins can also be used as diagnostic tools for the diagnosis of botulism. The transformed host cells can be used to analyse the effectiveness of drugs and agents which inhibit toxin effects. The vaccine currently used against botulism is dangerous and expensive to produce, and contains formalin, which is very painful for the recipient. Also, the vaccine is incomplete, in that only 5 of the 7 serotypes are represented in the formulation. The novel vaccine of overcomes these problems, as it is easily purified, and available in large quantities. It is also expressed in the lymph nodes for a better immune response. Sequences AAY77134-Y77139 represent
                                                                                                                                         Matches
                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel vaccines that induce a protective immune response against botulinum neurotoxin (BONT) serotypes A, B, C, D, E, F and G (BONTA-BONTG). The vaccine of the invention is novel recombinant DNA construct comprising a vector, and at least one nucleic acid fragment comprising a C-terminal heavy chain fragment (HC) from BONT serotypes A-G. In preferred embodiments of the invention, the vector is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulinum neurotoxin; heavy chain; BoNT; serotype F; C-terminal fragment; Venezuelan equine encephalitis virus replicon; VEE; botulism; vaccine; diagnosis; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   botulinum
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12-MAY-1999;
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                                                                                                                                                                                                                          Sequence
     401
                                                                    341
ADISIAKPEKIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-160827/14
                                                                  adisiakpekiiklirtsnsnnslgqiivmdsignnctmnfqnnnggnigllgfhsnnlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botulinum neurotoxin vaccine comprising a fragment from serotypes A-G, is used for inducing an immune response a
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                      these sequences had been optimised for codon usage for on in yeast. Note: This sequence is not given in the ation, but is decoded from the BONTF Hc DNA sequence given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pushko P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            botulinum
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99US-0133870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotoxin serotype F (BoNTF) C-terminal fragment.
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                                                                                                                                                       64.3%;
100.0%;
                                                                                                                                                       Score 92;
Pred. No.
                                                                                                                                       0;
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                                                                                                                                       Mismatches
                                                                                                                                                       DB 21;
8.7e-87;
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RESULT AABO4095 ID AAB XX

AAB04095 standard;

Protein; 419

0,

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AAW68399
ID
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                                                        Matches
                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat humans and other animals at risk of intoxication with clostridial toxin
                                                                                                                                                    recombinant toxins are used as immunogens for the production of vaccines and antitoxins that are useful in the treatment of humans and animals at risk of intoxication with clostridial toxin.
                                                                                                                                                                                          contamination. Preferred hosts for production or reproteins are E. coll, insect cells and yeast cells.
                                                                                                                                                                                                     derived from C. botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin contamination. Preferred hosts for production of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                Example 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thalley BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       botulism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OPHI-) OPHIDIAN PHARM INC
380 siggiivmdsignnctmnfqnnng 403
                            74 SLGQIIVMDSIGNNCTMNFQNNNG 97
                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                            448
                                                                                                                                                                                                                                                                                                                                                              Page 364-365; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          botulinum serotype F strain 202F (ATCC 23387).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              botulinum
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                     16.8%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F; intoxication; immunogen;
                                                                     DB 19;
2e-16;
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                                                                                  Length 448
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Search completed: August 15, 2002, 11:12:28 Job time: 320 sec
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                                                                                                                                                                                                                                                         Botulism neurotoxins are translated as a single 150 kDa polypeptide CC chain and then posttranslationally nicked, forming a dichain CC consisting of a 100 kDa heavy chain and a 50 kDa light chain which CR carboxy-terminal (HC) or amino-terminal (HM) portion of the heavy CC chain of botulinum neurotoxin (BONT) can be used in recombinant CC peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes CC protective immunity against botulinum neurotoxin, which causes CC organisms such as Escherichia coll or Pichhia pastoris. The use CC of recombinant nucleic acids are expressible in a recombinant CC organisms such as Escherichia coll or Pichhia pastoris. The use CC the need to culture large quantities of hazardous toxin-producing CC the need to culture large quantities of hazardous toxin-producing CC the need to culture large quantities of hazardous toxin-producing CC is also high and cost of production is lower. The nucleic acids can CC be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                  Matches
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12-MAY-1999;
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12-MAY-1999;
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12-MAY-1999;
29-JUL-1999;
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Clostridium botulinum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 8; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids encoding the carboxy or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA54489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-016048/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith LA, Byrne MP, Middlebrook JL, Lapenotiere H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
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                                                                               361 gnnctmnf 368
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                                                                                                                                            / Match 5.6%; Score 8; DB;
Local Similarity 100.0%; Pred. No. 6.9
pes 8; Conservative 0; Mismatches
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143
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T39345
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neurotoxin type F
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RESULT 2 \$33411 bothlinum neurotoxin typ C:Species: Clostridium b C:Date: 13-Jan 1995 #sec C:Accession: \$33411: \$31 R:Thompson, D.E.; Hutson FEMS Microbiol. Lett. IC A;Title: Nucleotide sequ A;Reference number: \$334 A;Accession: \$33411 A;Status: preliminary A;Melecule type: DNA A;Residues: 1-1268 <tho a;cross-references:="" embi<="" th=""><th>Query Matches Matches Qy 74 SI Db 1206 SI</th><th>RESULT 1 I40813 IAU813 REUROTOXIN type F - Clostridium botuling C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Date: 16-Aug-1996 #sequence_revision C;Accession: I40813; S48108 R;East, A.K.; Richardson, P.T.; Allawa; FEMS Microbiol. Lett. 96, 225-230, 199 A;Title: Sequence of the gene encoding A;Reference number: I40644 A;Accession: I40813 A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-1274 <res> A;Cross-references: GB.M92906; NID:914- R;Campbell, K.D.; Collins, M.D.; East, J. Clin. Microbiol. 31, 2255-2562, 199 A;Title: Gene probes for identification A;Reference number: S48108 A;Residues: S48108 A;Residues: S48108 A;Residues: S48108 A;Residues: GB-1002 <camd 634-1002="" <camd="" a;residues:="" c;keywords:="" c;superfamily:="" neurotoxin<="" tetanus="" th="" toxin=""><th></th><th>44444433333333333333333333333333333333</th></camd></res></th></tho>	Query Matches Matches Qy 74 SI Db 1206 SI	RESULT 1 I40813 IAU813 REUROTOXIN type F - Clostridium botuling C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Date: 16-Aug-1996 #sequence_revision C;Accession: I40813; S48108 R;East, A.K.; Richardson, P.T.; Allawa; FEMS Microbiol. Lett. 96, 225-230, 199 A;Title: Sequence of the gene encoding A;Reference number: I40644 A;Accession: I40813 A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-1274 <res> A;Cross-references: GB.M92906; NID:914- R;Campbell, K.D.; Collins, M.D.; East, J. Clin. Microbiol. 31, 2255-2562, 199 A;Title: Gene probes for identification A;Reference number: S48108 A;Residues: S48108 A;Residues: S48108 A;Residues: S48108 A;Residues: GB-1002 <camd 634-1002="" <camd="" a;residues:="" c;keywords:="" c;superfamily:="" neurotoxin<="" tetanus="" th="" toxin=""><th></th><th>44444433333333333333333333333333333333</th></camd></res>		44444433333333333333333333333333333333
um neurotoxin es: Clostridiu 13-Jan-1995 # sion: S33411; son, D.E.; Hut crobbol. Lett. : Nucleotide s ence number: S sion: S33411 s: preliminary ues: 1-1268 <7 -references: E	2 - 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	n type F - Cl : Clostridium 6-Aug-1996 #s on: 140813; S K.; Richards K.; Richards K.; Richards in: 140813 preliminary; e type: DNA s: 1-1274 ~es eferences: GB J. K.D.; Coll Microbiol. 31 Microbiol. 31 Seigene probes f ce number: S4 on: S48108 preliminary; e type: DNA s: 184108 s: 184108 preliminary; etype: DNA sis: 634-1002 < seferences: Exercises: Seigeneral		a a a a a a a a a a a a a a a a a a a
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barati -Jan-1995 #text; Allaway, D.; coding for Clost	re 24; DB 2; Length 12 ed. No. 1.3e-16; Mismatches 0; Indels	n 5-Aug-1996 #text_ D.; Collins, M.D ype F neurotoxin B/EMBL/DDBJ 56; PIDN:AAA23263 .K. of the botulinal hown	ALIGNMENTS	
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A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the s A;Reference number: A60027; MUID:90344918
A;Recession: A60027
A;Rocession: A60027
A;Rocession: A60027
A;Residues: 420-427 <GIM>
A;Residues: 420-427 <GIM>
A;Residues: 410-427 <GIM>
A;Residues: 420-427 <GIM>
A;Rote: this fragment was generated by proteolysis with Lys-C rather than with trypsin C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit ne C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the li C;Superfamily: tetanus toxin C;Superfamily: tetanus toxin C;Keywords: neurotoxin
C;Keywords: neurotoxin
F;1-422/Product: botulinum neurotoxin type E light chain #status predicted <HCH>
F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>
F;412-426/Disulfide bonds: #status predicted
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A; Residues: 1-176,'R',178-197,'C',199-339,'R',341-772,'I',774-962,'FE',965-966,'R',968-A; Residues: 1-176, 'R',178-197,'C',199-339,'R',341-772,'I',774-962,'FE',965-966,'R',968-A; Cross-references: EMBL:X62089; NID:940393; PIDN:CAAA3999.1; PID:940394
A; Experimental source: strain Beluga
A; Experimental source: strain Beluga
R; Binz, T.; Kurazzono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 616-982 <CAM>
A; Residues: 616-982 <CAM>
A; Residues: 616-982 <CAM>
A; Cross-references: EMBL:X70815; NID:9407786; PIDN:CAA50146.1; PID:9407787
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
B; Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem. Biophys. Res. Commun. 183, 107-113, 1992
A; Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum A; Reference number: JH0256; MUID:92181428
A; Accession: JH0257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-176, 'R', 178-252 <BIN>
A; Experimental source: strain Beluga
R; Gimenez, J.A.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
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J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurota
A;Reference number: A35294; MUID:90264400
A;Accession: B35294
A;Status: not compared with conceptual translation
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A;Tille: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxina; Reference number: S21178; MUID:92174922
A;Accession: S21178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the
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C; Date: 30
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C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S48103; MUID:94013372
A;Accession: S48107
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A; Residues: 1-1252 <WHE>
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es; Clostridium botulinum
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Oct-1999
sion: S21178; S48107; JH0257; B35294; A60027; S18111
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J. 3.1e-08;
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A;Map position: 4
A;Introns: 36/1; 59/3; 88/2; 116/1
C;Superfamily: Caenorhabditis elegans hypothetical
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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T27999
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AI1594
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C;Accession: AI1594
R;Glaser, P; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, E.; Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein lin1298 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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A; Gene: lin1298
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A;Residues: 1-67 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96529.1;
A;Experimental source: strain Clip11262
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A; Residues: 1-242 <WIL>
A; Cross-references: EMBL: Z83246; PIDN: CAB05842.1; GSPDB: GN00022; CESP: ZK795.1
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                                                                                                                                                                          A; Gene: CESP: ZK795.1
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56 IAKPEKI 62
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7; Conserv
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0; Mismatches
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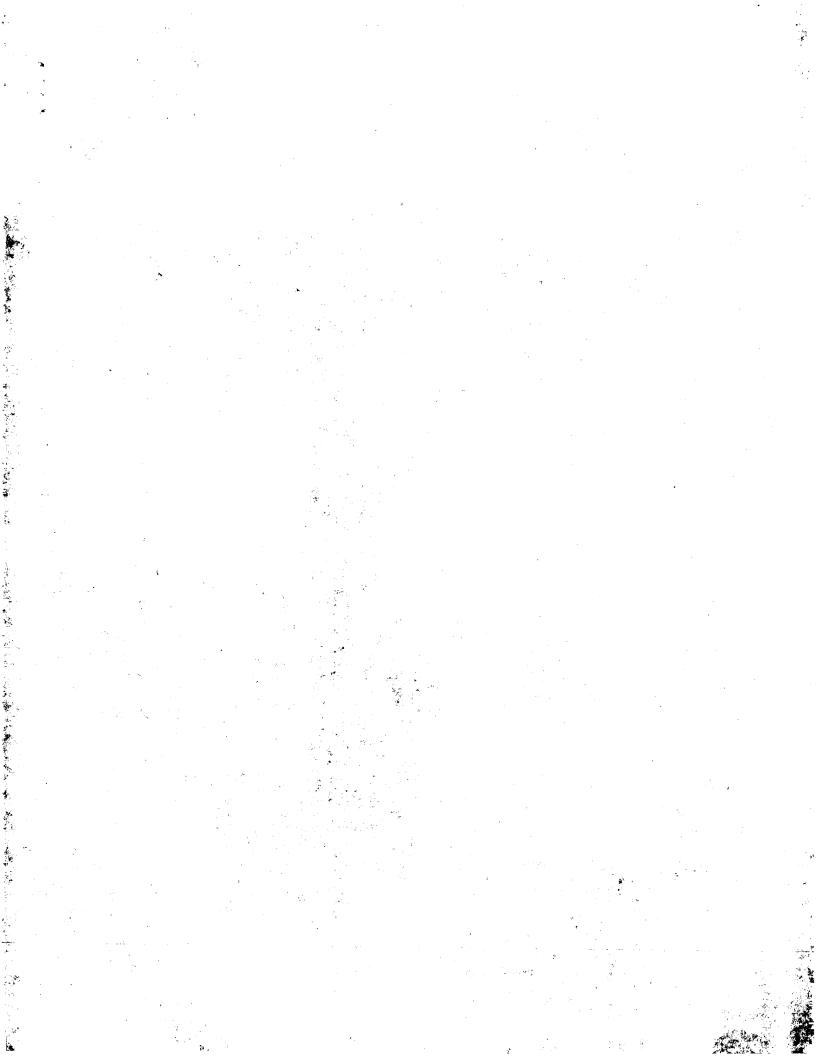
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dundinguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1186
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A;Molecule type: DNA
A;Residues: 1-259 GGLAS
A;Cross references: GB:AL592072; PIDN:CAC96126.1; PID:g16413344; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1544
pyridoxal kinase (pdxK) homolog - Lyme disease spirochete
C;Species: Borrella burgdorferi (Lyme disease spirochete)
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A;Molecule type: DNA
A;Molecule type: CNA
A;Residues: 1-259 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98973.1; PID:g16410298; GSPDB:GN00177
A;Experimental source: strain EGD-e
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C;Species: 1.7-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AG1186
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C;Superfamily: transcription sigma factor G; transcription initiation factor sigma katF
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Best Local
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Best Local
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                                                                                                                                               63 GNIGLLG 69
                                                                                                                                                                                                98 GNIGLLG 104
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                                                                                                                                                                                                                                                 Local Similarity es 7; Conserv
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Local Similarity 100.0%;
es 7; Conservative (
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o. 19;
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hypothetical protein C47B2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-OCT-1999 #sequence_revision 15-OCT-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Machado-Joseph disease MJDIa-like protein - Arabidopsis thaliana N;Alternate names: protein F24B22.90 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi
A;Reference number: A70100; MUID:98065943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: G70195 C;Accession: G70195 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Experimental source: clone C47B2 C;Genetics:
                                                                                                                              A;Reference number: Z19208
A;Accession: T1998
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Note: F24B22.90
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A; Residues: 1-280 <BLO>
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A; Accession: T47572
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A;Experimental source: strain B31
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A; Residues: 1-264 <KLE>
                                                     A; Molecule type: DNA
A; Residues: 1-347 <WIL>
A; Cross-references: EMB
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                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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Best Local
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                                                     EMBL: Z99709; PIDN: CAB16861.1; GSPDB: GN00019; CESP: C47B2.6
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100.0%; Pred. No. 20;
tive 0; Mismatches
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Pred. No.
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A;Gene: TM0447
C;Superfamily: phosphoribosylaminoimidazole carboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase
E;15-349/Domain: phosphoribosylaminoimidazole carboxylas
                                                                                                                                                                                                                                                                                                                                                                                               probable phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon diox c;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: H72374 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
                                                                                                                                                                                                                                                                 A:Title: Evidence for lateral gene transfer between Archaea and A:Reference number: A/2200; MUID:99287316
A:Accession: H72374
A:Status: preliminary
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A83636
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A;Map position: 1
A;Introns: 39/1; 115/3; 258/3; 296/3
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                       A;Cross-references: GB:AE001723; GB:AE000512; A;Experimental source: strain MSB8
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A; Residues: 1-380 < ARN>
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C.M.
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A; Residues: 1-375 <STO>
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Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                            Nature 399, 323-329, 1999
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Query Match
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Best Local
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107 YRLYADI 113
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nes 7; Conserv
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Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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Pred. No.
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                   Score 7;
Pred. No.
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Coulter, S.N.; Folger, K.R.;
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25;
                   DB 2;
. 27;
                                                                                            carboxylase carbon dioxide-fixation chain
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                                     Length 380;
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A.; Larbig,
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A:Molecule type: DNA
A:Residues: 1-387 <KID1>
R:Kidd, A.H.; Erasmus, M.J.
Virology 172, 134-144, 1989
Virology 172, 134-144, 1989
A:Title: Sequence characterization of the A:Reference number: A30336; MUID:89370295
A:Accession: A30336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 337-387 KID>
A;Residues: 337-387 KID>
A;Cross-references: GB:M60327; NID:g209932; PIDN:AAA42505.1; PID:g209933
A;Experimental source: strain FB585
R;Pienaziek, N.J.; Slemenda, S.B.; Pienazek, D.; Velarde Jr., J.; Luftig submitted to the EMBL Data Library, March 1990
A;Description: Characterisation of the early region E3 of the human ente: A;Reference number: S20688
A;Accession: S20695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: EMBL:X17016; NID:g58478; PIDN: A;Experimental source: strain Tak R;Kidd, A.H.; Erasmus, M.J.; Tiemessen, C.T. Virology 179, 139-150, 1990
A;Title: Fiber sequence heterogeneity in subgroup A;Reference number: A45352; MUID:91021015
A;Accession: A45352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S09217; A4535; S20695
R;Pieniazek, N.J.; Slemenda, S.B.; Pieniazek, D.; Velarde Jr., J.; Luftig, R.B. Nucleic Acids Res. 18, 1901, 1990
A;Title: Human enteric adenovirus type 41 (Tak) contains a second fiber protein A;Reference number: S09217; MUID:90245595
A;Accession: S09217
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41K fiber protein - human adenovirus 41
41K fiber protein - human adenovirus 41)
                                                                                                                                                                                                                                                                          A; Note: host Homo sapiens (man)
C; Date: 30-Jun-1990 #sequence_revision
C; Accession: A40048; A30336
                                                                                                                                                                                                                                                                                                                                           41K fiber protein - human adenovirus 40 C; Species: Mastadenovirus h40 (human adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-58 <PI25
A;Cross-references: EMBL:X52198; NID:g58660;
C;Superfamily: adenovirus fiber protein
                                                                                                                                                                                                                                  R; Kidd, A.H. submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords:
A; Molecule type: DN
A; Residues: 163-387
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A; Residues: 1-387 <PIE>
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                                                                                adenovirus 40
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28;
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hypothetical protein yerH - Bacillus subtilis
C;Datecles: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 **sequence_revision 05-Dec-1997 **text_change 20-Jun-2000
C;Catce: 05-Dec-1997 **sequence_revision 05-Dec-1997 **text_change 20-Jun-2000
C;Catcession: G69794
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C:; Broni, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A:; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
Na; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchyama,
T.; Winters, P.; Wipat, A.; Yamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchyama,
A.; Althors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033
A, Accession: G69794
A; Residues: 1-396 <KUNN
A; Residues: Schielich Schielich
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C;Superfamily: adenovirus fiber protein
C;Keywords: early protein
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C;Superfamily: Bacillus subtilis hypothetical protein yerH
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143
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COX1_SAJER
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Y884_CHLPN
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asi J., Link E., Cornille F., inn R., Niemann H.; innyAMP family by types D and in."; NHIBITING NEUROTRANGMITTER RONAL SYNAPSES, IS INTERNALIZED TO THE SAON INTO THE SPINAL CORD TIC AND PRESYNAPTIC NEURONS. IT Y ACTING AS A ZINC DROLYSIS OF THE 58-GLN- -LYS-59 Sis of proceins of the ravins, SNAP25 or syntaxin. No	botulinal neurotoxin gene and ypes B, E, and F.";	g components of botulinum of the gene coding for the Clostridium botulinum type F.";	COllins M.D., eurotoxin of Clostridium		TS	047189 erwinia car p25433 gallus gall p53177 saccharomyc p50668 choristoneu p50669 choristoneu p50670 choristoneu p50671 choristoneu p450072 haemophilus O9z774 chlamydia p 027860 methanobact O9pjll chlamydia m

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FIB2_ADE40
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PROSITE; PS00142; ZINC_PROTEASE; 1.

Neurotoxin; Transmembrane; Hydroclase; Metalloprotease; Zinc.

CHAIN 1 436

BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.

CHAIN 437 1274

BOTULINUM NEUROTOXIN F, HEAVY-CHAIN.

CHAIN 227 ZINC (CATALYTIC) (BY SIMILARITY).

METAL 227 ZINC (CATALYTIC) (BY SIMILARITY).

METAL 231 231 ZINC_(CATALYTIC) (BY SIMILARITY).
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SEQUENCE FROM N.A.
MEDLINE=93297140; PubMed=8517033;
Kidd A.H., Chroboczek J., Cusack S.,
"Adenovirus type 40 virions contain to Virology 192:73-84(1993).
                                                                                                                                            Davison A.J., Telford E.A., Watson M. "The DNA sequence of adenovirus type J. Mol. Biol. 234:1308-1316(1993).
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
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SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVI
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
FORMATION AND TOXIN BINDING, RESPECTIVELY.
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SUBCELLUAR LOCATION: SOCTETED.
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X70816; CAA50147.1;
P10845; 3BTA.
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S73676; AAC60475.1;
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24; Conservative
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(Rel. 33, Last of
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INTERCHAIN (PROBABLE).
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wo distinct fibers.";
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RESULT 3
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EMBL; M28822; AAA03233.1; -.
PIR; A40048; ERADY4.
InterPro; IPR000939; Adeno_fiber2.
InterPro; IPR000978; Adeno_fiber_knob.
InterPro; IPR000931; Adeno_fiber.
Pfam; PF000541; adeno_fiber; 1.
Pfam; PF00508; adeno_fiber; 5.
PRINTS; PR00307; ADENOVSFIBRE.
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01-AUG-1990
01-NOV-1995
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CONFLICT 22
SEQUENCE 387
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Nucleic Acids
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Human adenovirus type 4.
Viruses; dsDNA viruses,
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-!- FUNCTION: RECOGNIZES THE CELL RECEPTOR; SERVES AS BETWEEN THE ADENOVIRUS CAPSID AND THE HOST CELL RE-!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                    -i- FUNCTION: RECOGNIZES THE CELL RECEPT
BETWEEN THE ADENOVIRUS CAPSID AND TH
-i- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                       Kidd A.H., Erasmus M.J., Tiemessen C.T.; "Fiber sequence heterogeneity in subgroup Virology 179:139-150(1990).
                                                                                                                                                                                   MEDLINE=90245595; PubMed=2336370; Pieniazek N.J., Slemenda S.B., Pieniazek
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SEQUENCE OF 167-387 FROM N.A.
MEDLINE-89370295; PubMed-2773314;
                                                                                         MEDLINE=91021015; PubMed=2219717;
                                                                                                        STRAIN-FB585;
                                                                                                                 SEQUENCE OF
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                                                                     adenoviruses.";
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CRBA_DROME
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A ABEL T., Bhatt R., Maniatis T.;

T A Drosophila (REB/AFF transcriptional activator binds to both fat T a Drosophila (REB/AFF transcriptional activator binds to both fat T body and liver-specific regulatory elements.";

L Genes Dev. 6:466-480(1992).

C -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO FAT BODY-SPECIFIC CENHANCERS OF ALCOHOL DEHYDROGENASE (Ah!) AND YOLK PROTEIN GENES.

C BBF-2 MAY PLAY A ROLE IN FAT BODY GENE EXPRESSION. IT BINDS THE CONSENSUS SEQUENCE 5'T(A/C)NACGTAN(T/G)C-3'.

C -!- SUBBURIT: MAY BIND DNA AS HETEROLIMERS WHIT OTHER BZIP PROTEINS.

C -!- SUBGLICITY: IN ALL CELL TYPES EXAMINED.

C -!- SUBCLICITY: IN ALL CELL TYPES EXAMINED.
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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P29747;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
CYCLIC-AMP response element binding protein A (Box B binding factor-2)
(BBF-2).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREBA OR BBBF2
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InterPro; IPR000978; Adeno_fiber_knob.
InterPro; IPR000931; Adeno_fibre.
Pfam; PF00541; adeno_fiber; 1.
Pfam; PF00608; adeno_fiber2; 5.
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EMBL;
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X64429; CAA45771.1; -.
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NCE 387 AA; 41397 MW; 8652E785276573C7 CRC64;
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Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
o. 8.7;
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Best Local
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01-APR-1993
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                          STRAIN=S288C / AB972;
MEDLINE-94478003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Fulton L., Gattung S., Geisel C., Kirsten J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Riffin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0004396; CrebA.
InterPro; IPR001871; bZIP.
Pfam; PF00170; bZIF; 1.
SMART; SM00338; BRLZ; 1.
PROSSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; Activator; DNA-binding; Nuclear DNA_BIND 442 462 BASIC MOTIF.
DNA_BIND 442 462 BASIC MOTIF.-ZIPPER.
DOMAIN 468 503 LEUCINE-ZIPPER.
DOMAIN 468 503 LEUCINE-ZIPPER.
SEQUENCE 515 AA; 56528 MW; 0E08FB9655200223 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST
                                                                                            Science 265:2077-2082(1994),
1- FUNCTION: ACTS AS A SUPPRESSOR OF MITOCHONDRIAL SPLICING
DEFICENCIES WHEN OVERSYPRESSED. COULD BE A NON-ESSENTIAL
COMPONENT OF THE MITOCHONDRIAL SPLICING MACHINERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                "The NAM8 gene in Saccharomyces cerevisiae encodes a protein with purtative RNA binding motifs and acts as a suppressor of mitochondrial splicing deficiencies when overexpressed."; mol. Gen. Genet. 233:136-144(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAM8 OR MRE2 OR YHR086W.
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
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Slonimski P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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PIR; A42140; A42140.
TRANSFAC; T01603; -.
                                                                                                                                                                             "Complete nucleotide sequence of Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                Leem S.-H., Hayashi A.,
Submitted (JUN-1992) to
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ekwall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92293106; PubMed=1603056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
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                                                               SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM)
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
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(Rel. 31, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%;
Conservative
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update) annotation update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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   restrictions
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EMBL; D11461; BAA02016.1; -
EMBL; U00060; AAB68928.1; -
PIR; S22439; S22439.
PIR; S46720; S46720.
SGD; S0001128; NAM8
InterPro; IPR000504; RRM.
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Myuyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Nguyen D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
                 Bailey C.C., Younkins R., Huang W.M., Bott K.F.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME
SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.
PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLIC
OF A CIRCULAR DNA MOLECULE (BY SIMILARITY).

-!- SUBUNIT: COMPOSED OF TWO SUBUNITS: PARC AND PARE.
-!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
-!- SIMILARITY: STRONG, WITH THE A SUBUNIT OF GYRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBT TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P47446; Q49377;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Topoisomerase IV subunit A (EC 5.99.1.-).
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                                                                                                                                                                                                                                              SEQUENCE OF 1-479 FROM N.A. STRAIN-ATCC 33530 / G-37;
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lan email t
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242
385
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Pred. No.
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Best Local 9
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01-JUN-1994
01-JUN-1994
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Topoisomerase;
ACT_SITE 122
CONFLICT 261
                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                      Physcomitrella patens (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00521; DNA_topoisoIV; SMART; SM00434; TOP4c; 1. Topoisomerase; Isomerase; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              Phytochrome
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the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                            388 KIIKLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KIIKLIR
                                                                                                                           BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U39700; AAC71422.1;
U25549; AAC43991.1;
P09097; 1AB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MG204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002205; DNA_topoisoIV
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261
781 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                     29, Created)29, Last sequence up41, Last annotation
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88512
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100.0%;
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P -> R (IN RE
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Pred. No.
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F14319CEE305B437
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16;
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Best Local
                 SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M.G., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Nguyen D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00989; ras, ...
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
Pfam; PF00512; signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_
Transcript
                                                                                                                                                                                                                                                              049413; 049365;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updato)
                                                                                                                                                                                                  Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                               protein 1).
HMW1 OR MG312
                                                                                                                                                                                                                                                        Cytadherence high
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SMART; SM00091;
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SMARR; SM00387; HATPASE
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PRINTS; PR01033;
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PIR; S37206; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE OF 721-847 FROM N.A.
                                                                                                                                                                                NCBI_TaxID=2097
                                                                                                                                                                                         Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                       HMW1_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR001294; Phytochrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    h 4.9%; Score 7; DB:
Similarity 100.0%; Pred. No. 22
7; Conservative 0; Mismatches
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IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig.
IPR003661; His_kinA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                       STANDARD;
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PAS; 2.
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815
1115
321
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CHROMOPHORE (BY S
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                       protein 1 (Cytadherence accessory
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o. 22;
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BXE_CLOBO
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Matches 7
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1. Bacteriol. 175:7918-7930(1993).

2. Bacteriol. COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH

1. FUNCTION: COMPONENT OF THE WALL-LESS MYCOPLASMA. THIS

CYTOSKELETON LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HMW

PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTI

IN THE MYCOPLASMAL MEMBRANE AT THE ATTACHMENT ORGANELLE (BY

SIMILARITY).

SIMILARITY.

1. SUBBELLILIAR LOCATION: LOCALIZES SPECIFICALLY TO THE ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BXE_CLOBO STANDARD; PRT; 1250 AA.
000496;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JWR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BONT/E)
                                                                                           SEQUENCE FROM N.A. MEDILINE-92174922; PubMed=1541280; MEDILINE-92174922; PubMed=1541280; Whelan S.M., Elmore M.J., Bodsworth N.J., Atkinson T., Minton N.P.; "The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                                                                                         MEDLINE-92181428; PubMed-1543481;
Poulet S., Hauser D., Quanz M., Miemann H., Popoff M.R.;
Poulet S., Hauser D., Quanz M., Miemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium
botulinum type E (strain Beluga) and Clostridium butyricum (strain
ATCC 43181 and ATCC 43755).",
Biochem. Biophys. Res. Commun. 183:107-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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MEDLINE-94075230; Pubmed-0253680;
Peterson S.N., Hu P.-C., Bott K.F., Hut
"A survey of the Mycoplasma genitalium
                SEQUENCE OF 1-251 FROM N.A. MEDLINE=90264400; PubMed=21
                                                                                     gene.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum.
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                                                                   Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1491;
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Kurazono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ce; Structural protein; 1139 AA; 130531 MW;
                                                                   204:657-667(1992).
H., Wille M., Frevert J.,
                PubMed=2160960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9%; 5c.
100.0%; Pr
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o. 22;
Wernars K.,
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by using random
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Niemann
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EMBL;
PIR; I
PIR; I
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 InterPro; IPR000395;
InterPro; IPR000130;
Pfam; PF01742; Peptic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION OF SUBSTRATE.
MEDLINE=94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Benfenati F., Wilson M.C., Montecucco C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gimenez J.A., Dasgupta B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-13.
MEDLINE-85197963;
                                         MEROPS; M27.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94063091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteolysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION OF SUBSTRATE.
MEDLINE=94063091; PubMed=8243676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                        neuroexocytosis apparatus, synaptobravins, SNAP25 or synt detected action on small molecule substrates.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (I HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHAFORWATION AND TOXIN BINDING, RESPECTIVELY.
SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FOR BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
SIMILARITY: BELLONGS TO PEPTIDASE FAMILY M27.
                                                  A60027; A60027.
B35294; B35294;
JH0257; JH0257;
S08575; S08575;
S18111; S18111;
S21178; S21178;
S21178; S21178.
                                                                                                                                                                                                                                                                                                                                                                                                                                ENDOPEPTIDASE THAT CATALYZES THE HYDROI 181 BOND IN SNAP-25.
CATALYTIC ACTIVITY: Limited hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEEDLYSIS OF SNAP-25 by types E and A botulinal neurotoxins.";
Biol. Chem. 269:1617-1620(1994).
FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNAL AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete sequence of botulinum neurotoxin type A and comparison
  other clostridial neurotoxins.";
iol. Chem. 265:9153-9158(1990).
                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the
                                                                                                                                               X62089; CAA43999.1;
X62683; CAA44558.1;
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00395; Bontoxilysin.
00130; Zn_MTpeptdse.
Peptidase_M27; 1.
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trypsin nicks
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hyamoorthy V., Dasgupta B
id sequences of botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2116911;
                                                                                                                                                                                                                              institutions as long
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ks and homology with tetanus
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                                                                                                                                                                                                                          There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                of proteins
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RESULT 10
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Best Local
                                                                                                                                                                                                                                         STRAIN-ATCC 43181, AND ATCC 43755;

MEDLINE-92181428; PubMed=1543481;

Poulet S., Hauser D., Quanz M., Niemann H., Popof

"Sequences of the botulinal neurotoxin E derived
botulinum type E (strain Beluga) and Clostridium

ATCC 43181 and ATCC 43755).";
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METAL
ACT_SITE
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ProDom; I
PROSITE;
                                                                                      Gimenez J.,
                                                                                                                                                                                                                                                                                                                                                                               Botulinum neurotoxin (Bontoxilysin E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1206 NIGLLGF 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                      Gimenez J., Foley J., Dasgupta B.R.; "Neurotaxin type E from Clostridium partial sequence and comparison."; FASEB J. 2:A1750-A1750(1988).
                                                                                                                                 Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                   SEQUENCE OF 1-251 FROM N.A. STRAIN=BL6340;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 43181,
                                                                                                                                                                                                                                                                                                                                                          Clostridium butyricum Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993
01-MAR-2002
                                                                                                 STRAIN=5262;
                                                                                                                                                                                        MEDLINE=91237316; PubMed=2033376;
                                                                                                                                                                                                                                     Biochem.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1492;
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INIT_MET
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FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNAL AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL HEERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity
7; Conserv
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PD001963;
;; PS00142;
                                                                                                             OF,
                                                                                                                                                                                                                                    Biophys.
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AA; 143712
                                                                                                                                                                                                                                                                                                                                                                                26, Created)
26, Last sequence update)
41, Last annotation update)
xin type E precursor (EC 3.4.
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                                                                                                                                                                                                                                    Res.
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ZINC_PROTEASE;
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                                                                                                                                                                                                                                    Commun.
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BOTULINUM NEUROTOXIN E,
2INC (CATALYTIC) (BY SIM
PY SIMILARITY:
2INC (CATALYTIC) (BY SIN
INTERCHAIN (PROBABLE).
R -> G (IN REF. 2).
C -> S (IN REF. 2).
C -> S (IN REF. 2).
FE -> L (IN REF. 2).
FE -> LQ (IN REF. 2).
R -> A (IN REF. 2).
R -> A (IN REF. 2).
R -> A (IN REF. 2).
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                                                                                                                                                                                                                                    183:107-113(1992).
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D9FCE26DDA041EB4
                                                                             botulinum
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24;
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N E, HEAVY-CHA:
Y SIMILARITY):
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                                                                          butyricum
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HEAVY-CHAIN
                                                                                                                                                                                                                                                                     Clostridium
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HE SPINAL CORD
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RESULT 1:
V05K_BPT4
ID V05K,
AC 9392:
DT 01-FP
DT 01-FP
DT 01-FP
DT 01-FP
DT 01-FV
DF 14-FV
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Best Local
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PIR; S16145; S16145.
HSSP; P10845; 3BTA.
Mzhavia N., Marusich E., Djavakhishvili T., Neitzel J., Peterson S., Awaya M., Eidermiller J., Candad D., Tracy J., Gailbreath K., Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M.; "The 10.7 kb 'nonessential' region of bacteriophage T4 between the
                                                                                                                                                                                                                                                                                                              Bacteriophage T4.
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 7.6 kDa protein in mobb-ri intergenic region.
Y05K OR MOBD.3_OR TK.-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
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                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                    T4-like phages
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CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVELE THE N.AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.
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BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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K -> M (IN REF. 2).
W; 8171B5B2C2312857 CRC64;
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b. 24;
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                           "Purification and reconstitution of the electron transport components for 6-deoxyerythronolide B hydroxylase, a cytochrome P-450 enzyme of macrolide antiblotic (erythromycin) blosynthesis.";

J. Bacteriol. 170:1548-1553(1988).

1- FUNCTION: FERREDOXIN ARE IRON-SULFUR PROTEINS THAT TRANSFER ELECTRONS IN A WIDE VARETY OF METABOLIC REACTIONS.

1- COFACTOR: BINDS 1 4FE-4S CLUSTER AND A 3FE-4S CLUSTER.

1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.

1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institution as long as its content is in no way not be the proposity of the statement of the content is in no way not be supposed the statement of the content is in no way not be supposed the statement of the content is not way and the statement is not the content of the content is not way and the statement of the content is not way and the statement is not way the statement of the content is not way the statement is not way the statement of the content is not way the statement way the statement is not way the statement is 
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01-MAR-1992
01-OCT-1996
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P24496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharopolyspora erythraea (Streptomyces erythraeus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G. Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; "Bacteriophage T4 genome analysis."; "Batteriophage T4 genome analysis.";
use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91276248; PubMed=2055472;
Donadio S., Hutchinson C.R.;
"Cloning and characterization of the Saccharopolyspora erythraea fdxA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharopolyspora.
NCBI_TaxID=1836;
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SEQUENCE 64 AA; 7605 MW; 89E2AF66EE86CCE0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shafiee A., Hutchinson C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-15.
MEDLINE=88169474; PubMed=3127376;
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Gene 100:231-235(1991).
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(Rel. 21, Last sequence up)
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    and for commercial
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01-APR-1993 (Rel. 25, I
01-NOV-1997 (Rel. 35, I
Cytochrome c oxidase po
COXI OR COI.
                                                                                                                                                                                                                                                         "Phylogenetic relationships of neopterygian fishes, inferred mitochondrial DNA sequences,",
Mol. Biol. Evol. 8:819-834(1991).

11- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RECHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SU
S FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI I IS
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF S
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED B
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Actinopterygii; Neopterygii; Teleos:
Protacanthopterygii; Salmoniformes;
NCBI_TaxID=8032;
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P29653;
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                                                                                                     CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
c + 2 H(2)O.
PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                           European Bioinformatics Institute.
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                                      SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
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PR00354; 7FE8SFRDOXIN.
; PS00198; 4FE4S_FERREDOXIN;
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an email to license@isb-sib.ch).
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RESULT 14
Y884_CHLPN
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30-MAY-2000 (Rel. 39,
16-OCT-2001 (Rel. 40,
Hypothetical protein (
CPN0884 OR CP0982 OR (
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Q9Z722; Q9C
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SEQUENCE
                        Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kisl
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa
"Comparison of whole genome sequences of Chlamydia
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                               MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Olinger L., Grimwood J., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae (Ch
Bacteria; Chlamydiales;
NCBI_TaxID=83558;
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Pfam; PF00115; COX1; 1.
PROSITE; PS00077; COX1; 1.
                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                                                                                         Gwinn M., Nelson W., DeBoy
Eisen J., Fraser C.M.;
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HSSP; P00396; 10CC.
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                                                                                                                                                                                                                                                                                                                                  Grimwood J., Davis R.We genomes of Chlamydia 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain; Inner
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RESULT 15
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Q17005;
   Hydrolase;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of a lysozyme gene from the malaria vector mosquito, Anopheles gambiae.",
Gene 174:239-244(1966).
-!- FUNCTION: LYSOZYMES HAVE PRIMARILY BACTERIOLYTIC FUNCTION; THOSE IN TISSUES AND BODY FLUIDS ARE ASSOCIATED WITH THE MONOCYTE-MACROPHAGE SYSTEM AND SHANCE THE ACTIVITY OF INMUNAGEBYS.
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.
-!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Lysozyme precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).
Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Hypothetical protein; Transmembrane; Complete proteome.

TRANSMEM 30 50

POTENTIAL.

SEQUENCE 117 AA; 13152 MW; 45D3D3AC8B9E11A2 CRC64;
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MEDLINE=97045819; PubMed=8890741;
Kang D., Romans P., Lee J.Y.;
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PRINTS; PR00135; LYZLACT.
SMART; SM00263; LYZLACT.
PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
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Pfam; PF00062; lys; 1.
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   Glycosidase; Bacteriolytic enzyme; Signal.

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051665 borrelia bu
097vc3 sulfolobus
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5: sp_inverteb:
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6: sp_manmal:*
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8: sp_organel:*
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
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sp_virus:*
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sp_bacteriap:*
sp_archeap:*
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                                                                  STRAIN=LANGELAND; when the strength of the botulinum neurotoxin type F gene clusters in "Analysis of the botulinum neurotoxin type F gene clusters in proteolytic and nonproteolytic Clostridium botulinum and Clostridium barati.";

Curr. Microbiol. 37:262-268(1998).
                                                                                                                                                                                                                                                                                       057236; 045863; 045863; 057238; 045863; 045863; 045863; 045863; 01.NOV-1996 (TIEMBLIEL 01, Last sequence update) 01.NOV-1996 (TIEMBLIEL 01, Last sequence update) 01.UN-2001 (TIEMBLIEL 1, T). Last annotation update DOTULINUM NEUROTOXIN TYPE F (BONT/F PROTEIN).
                                                                                 SEQUENCE OF 635-1000 FROM N.A.

STRALNE-NCTC 1028;

MEDLINE-94013372; PubMed-8408542;

Campbell K., East A.K., Collins M.D.;

"Gene probes for identification of the botulinal neurotoxin specific identification neurotoxin types B, E, and F.";

J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                          Clostridium botulinum.
Bacteria; Firmicutes;
Clostridium.
NCBI_TaxID=1491;
                                                                                                                                                                                          STRAIN-NCTC 10281;
Hutson R.A., Collins M.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Elmore M.J., Bodsworth N.J., Whelan S.M., Minton N.P.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             SEQUENCE FROM N.A.
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Q9YVU6
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Q913v4 porcine gam Q9bhy8 leishmania Q93zt8 arabidopsis Q93u59 candidatus Q9c469 schizosacch O51274 borrelia b

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Database :

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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOm; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNB SEQUENCE 1280 AA; 147487 MW; D0F
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EMBL; L35496; AAA23210.1;
EMBL; CAA50152.1;
EMBL; X99064; CAA67512.1;
EMBL; X99064; GAA67512.1;
HSSP; P10845; 3BTA.
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Q9ZAJ5;
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Clostridium botulinum
rirmicutes;
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EMBL; Y13631; CAA73972.1; -.
HSSP; P10845; 3BTA.
MEROPS; M27.002; -.
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InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01742; Peptidase_W27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSTIE; PS00142; ZINC_PROTEASE; UI
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MEDLINE=98440323; PubMed-976710;
Santos-Buelga J., Collins M.D., E
"Characterization of the genes en
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genes encoding the Botulinum neurotoxin
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EMBL; X6826; CAA48329.1; -.

HSSP; P10845; 3BTA.

MEROPS; M27.002; -.

InterPro; IPR000395; Bontoxilysin.

InterPro; IPR000395; Bontoxilysin.

InterPro; IPR000130; Zn_MTpeptdse.

Pfam; PF01742; Peptidase_M27; 1.

PRINTS; PR00760; BONTOXILYSIN.

PRODOm; DD001963; Bontoxilysin; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

SEQUENCE 1268 AA; 145513 MW; 963040091AC15ED2
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Q1-NOV-1996 (TrEMBLrel. 01, C:
01-NOV-1996 (TrEMBLrel. 01, L:
01-OCT-2000 (TrEMBLrel. 15, L:
01-OCT-TAINM NEUROTOXIN TYPE E (
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q45851;
Q45851;
                                                              EMBL;
                                                                             SEQUENCE FROM N.A.
STRAILNESSE E, HAZEN 36208 (ATCC 9564);
STRAILNESSE E, HAZEN 36208 (ATCC 9564);
MEDLINESSE E, PubMed-8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                           Q45862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium baratii.
Bacteria; Firmicutes;
Clostridium.
                                                                                                                                                                                                          Clostridium botulinum. Bacteria; Firmicutes;
                                                                                                                                                                                              Bacteria; F. Clostridium
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Richardson P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                          Neurotoxin.
NON_TER
                                                     EMBL; X70815; HSSP; P10845;
                                                                                                                                                                                  NCBI_TaxID=1491;
                                                                                                                                                                                                                                    BONT/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93252228;
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               NON_TER
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                                                     CAA50146.1;
3BTA.
   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8486245;
tson R.A., East
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Pred. No.
   0810595B3A865570 CRC64;
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                                                                                                                                                                                                                                                            sequence update) annotation updat
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963040091AC15ED2 CRC64;
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                                                                                                                                                                                                           group; Clostridiaceae;
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Best Local :
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Best Local
                                                                                                                                                                                                                        Karasawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9K395 PRELIMINARY; PRT; 1251 AA.
O9K395; O1-OCT-2000 (TIEMBLrel. 15, Created)
O1-OCT-2000 (TIEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TIEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=TYPE E, VH (DOLMAN);
STRAIN=TYPE E, VH (DOLMAN);
MEDLINE-94013372; PubMed-8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and the probes for identification of the botulinal neurotoxin types B, E, and F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q45861;
Q45861;
SEQUENCE FROM N.A.
STRAIN-LCL 155 (KZ 1885);
Wang X., Maegawa T., Kozaki S., Ts
Kato H., Nakamura S., Karasawa T.;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=LCL 095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium butyricum. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIE1. 01, Created)
01-NOV-1996 (TIEMBLIE1. 15, Last Sequence update)
01-CCT-2000 (TIEMBLIE1. 15, Last annotation updat
BOTULINUM NEUROTOXIN TYPE E (FRAGMENT).
                                                                                                                                                                             "C. butyricum (LCL 095) gene for type E botulinum toxin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BONT/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE E BOTULINUM TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specific identification of neurotoxin types B, J. Clin Microbiol. 31:2255-2262(1993). EMBL; x70818; CAASO149-1; -. HSSP; P10845; 3BTA.
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Bacteria; Firmicutes; Bacillus/Clostridium
Clostridium.
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367
367 AA;
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                                 Tsukamoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
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                                 Gyobu Y., Yamakawa K.,
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"C. butyricum (ICL 063) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL. AB037714; BaB03522.1; -... EMBL, AB037704; BAB03512.1; -.. EMBL; AB037705; BAB03513.1; -.. EMBL; AB037706; BAB03513.1; -.. EMBL; AB037707; BAB03515.1; -.. EMBL; AB037707; BAB03515.1; -.. EMBL; AB037707; BAB03515.1; -.. EMBL; AB037709; BAB03518.1; -.. EMBL; AB037709; BAB03518.1; -..
                                                                                                                                                                                                                                                 "C. butyricum (KZ 1891) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C. butyricum (KZ 1889) gene for type E botulinum toxin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                    Karasawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2000) to [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "C. butyricum (KZ 1898) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "C. butyricum (KZ 1897) gene for type E botulinum toxin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "C. butyricum (KZ 1899) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   Karasawa T
"C. butyri
                                                                                                                                                                                  Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
                                                                                                                                                                                                 STRAIN-LCL
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=KZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
Karasawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-KZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "C. butyricum (KZ 1887) gene for type E botulinum toxin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
Karasawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
Karasawa T.;
"C. butyricum (KZ 1886) gene for type E bofulinum forin ".
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Karasawa T.;
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submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                  Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
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STRAIN-KZ 1886;
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nitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Q45894 PKELLILL...
Q45894; P77780;
Q45894; P77780;
Ol-NOV-1996 (TrEMBLrel. 01, Created)
Ol-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ol-DEC-2001 (TrEMBLREL. 19, Last annotation update)
Ol-DEC-2001 (TrEMBLREL. 19, Last annotation update)
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InterPro; IPRO0030; Zn_MTpeptdse.
Pfam; PF01742; Peptidse_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOm; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNK
SEQUENCE 1251 AA; 143751 MW; 202
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01-MAR-2001
01-MAR-2001
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TYPE E BOTUL
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EMBL; AB037712; B.
EMBL; AB037713; B.
EMBL; AB037713; B.
HSSP; P10845; 3BT.
MEROPS; M27.002;
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PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1255 AA; 143918 MW; 1B557B9D85CD8E4D
                                                                                                                                                                                                                                                                     InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
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EMBL;
HSSP;
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Yamakawa K., Oguma K., Sakaguc
"Genetic Analysis of Type E Bo
butyricum Strains.";
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l1; Conservative
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BAB03520.1;
BAB03521.1;
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Sakaguchi Y., Nakamur
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16,
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2021F4E427070296
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0.018;
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0.018;
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a S.;
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"Molecular characterization of two for
components of Clostridium botulinum ty
FEBS Lett. 376:41-44(1995).
EMBL; X73423; CAA51824.1; -.
EMBL; X87974; CAA63551.1; -.
EMBL; X87974; CAA61234.1; -.
EMBL; X87974; CAA61234.1; -.
EMBL; D67030; BAA11051.1; -.
HSSP; P10845; 3BTA.
InterPro; IPR000395; Bontoxilysin.
Pfam; PF01742; Peptidas_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Q45846;
Q45846;
Q1-NOV-1996
Q1-NOV-1996
Q1-OCT-2000
                                 SEQUENCE FROM N.A.
STRAIN-TYPE B, NON-PROTEOLYTIC 21
MEDLINE-94013372; PubMed-8408542;
Campbell K., East A.K., Collins M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
ProDom;
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East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94143603; PubMed=8310180; Willems A., East A.K., Lawson P.A., Collins M.D.; "Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison wiother clostridial neurotoxins."; Res. Microbiol. 144:547-556(1993).
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Clostridium botulinum.
Bacteria; Firmicutes;
Clostridium.
                                                                                                                                                                                                                                   Bacteria; Fi
Clostridium
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STRAIN-TYPE A NIH;
MEDLINE-96096783; PubMed-8521962;
"Gene
                                                                                                                                                                                                                                                                                                       Clostridium
                                                                                                                                                                                                                                                                                                                                                                       BOTULINUM
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SEQUENCE
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                                                                                                                                                                                                 NCBI_TaxID=1491;
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PD001963;
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   t A.K., Collins identification
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      the
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   botulinal
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   neurotoxin
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RESULT
Q9X708
ID Q9X708
AC Q9
AC Q9
AC Q9
AC Q9
AC Q9
CO Q0

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                                                                                                                                                                                                                                                                                Q9X708;
                                                                                                                                                                                   01-NOV-1999 (TREMBLrel. 12, Created)
01-NOV-1999 (TREMBLrel. 12, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
BOTULINUM NEUROTOXIN TYPE B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-TYPE B, NON-PROTECLYTIC EKLUND 2B (COLWORTH 229);
STRAINE-94013372; PubMed-8408542;
MEDLINE-940413372; PubMed-8608542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-NOV-1996 (TREMBLrel. 15, Last annotation update)
BOTULINUM NEUROTOXIN TYPE B (FRAGMENT).
SEQUENCE FROM N.A.
MEDLINE=99343691; PubMed=10413679;
                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                     BONT/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BONT/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q45848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X70814; CAA50145.1; HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific identification of neurotoxin types B, E, J. Clin. Microbiol. 31:2255-2262(1993).
                                                                        NCBI_TaxID=1491;
                                                                                                                                             Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1491;
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                                                                                                  lostridium
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8; Conserv
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71
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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42131 MW; A2E0FFFC81F9533D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
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100.0%; Pro
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                                                                                                                  Bacillus/Clostridium group; Clostridiaceae;
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Pred. No.
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5. 7.1;
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o. 7.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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RESULT 13
Q9ZAJ8
ID Q9ZAJ8
AC Q9ZAJ8
DT 01-MAX
DT 01-MAX
DT 01-DEC
DE BONT F
GN BONT.
GOS Clostr
OC Clostr
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Best Local :
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NON_TER
SEQUENCE
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Schiavo G.
                                                                                            Clostridium botulinum Bacteria; Firmicutes;
                                                                                                                                                                                               Q9ZAJ8 PRELIMINARY; PRT; 1291 AA.
Q9ZAJ8; O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach, Ehrlich S.D., Sorokin A., "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.", Genome Res. 11:731-753(2001).

Genome Res. 11:731-753(2001).

EMBL; AE006392; AAK05715.1;
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09CF64; O1-GT-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence of the control of the contr
  SEQUENCE FROM N.A.
                                                                          Clostridium
                                                                                                                                                                             BONT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 1072 AA;
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STRAIN-IL1403;
MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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J. Cell Sci. 112:2715-2724(1999).
EMBL; AJ242628; CAB43706.1; -.
HSSP; P10845; 3BTA.
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                                            NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         712 SSKPSEVN 719
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les 8; Conservative 0;
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8; Conser
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441
441 AA;
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52772 MW;
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100.0%; Pred. N
                                                                                                  Bacillus/Clostridium group; Clostridiaceae;
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Last annotation updat
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RR STRAIN-ERLUND 17B ATCC25765;

RX MEDLINE-94122659; Pubmed-7764370;

RY Clostridial neurotoxins.";

RY CLOSTRIDIAL COLLINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

CC PUBLEASE. IT BINDS TO PERTHERAL NEURONAL SYNAPSES, IS INTERNALIZED

CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

CC ENDOPEPTIDASE THAT CLEAVES SYNAPTORREVIN-2.

CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

CC INHIBITS NEUROTRANSMITTER CHANNEL OF THE HEAVY CHAIN MEDIATE CHANNEL

CC INHIBITS NEUROTOXIN BINDING, RESPECTIVELY.

CC INHIBITS NEUROTOXIN BINDING, RESPECTIVELY.

CC INHIBITS NEUROTOXIN BINDING, RESPECTIVELY.

CC INHIBITS NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

CC NEUROTOXIN.

CC INHIBITS NEUROTOXIN BINDING NEUROTOXINS AND WITH TETANUS

CC NEUROTOXIN.
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01-JUN-2001
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                                                                                    EMBL; X71343; CAA50482.1;
HSSP; P10845; 3BTA.
MEROPS; M27.002; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
BOTULINUM NEUROTOXIN TYPE B (EC 3.4.24.-) (BONT/B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; Zn_MTpeptdse. Pfam; PF01742; Peptidase, M27; 1. PRINTS; PR00760; BONTOXILYSIN. ProDom; PD001963; Bontoxilysin; 1. PROSITE; PS00142; ZINC_PROTEASE; U SEQUENCE 1291 AA; 150840 MW; E
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EMBL; Y13630; CAA73968.1; -.
HSSP; P10845; BBTA.
MEROPS; M27.002; -.
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MEDLINE=98440323; PubMed=9767710;
Santos-Buelga J., Collins M.D., East A.K.;
"Characterization of the genes encoding the Botulinum neurotoxin
           Pfam;
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                                   InterPro; IPR000395;
InterPro; IPR000130;
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00130; Zn_MTpeptdse.
Peptidase_M27; 1.
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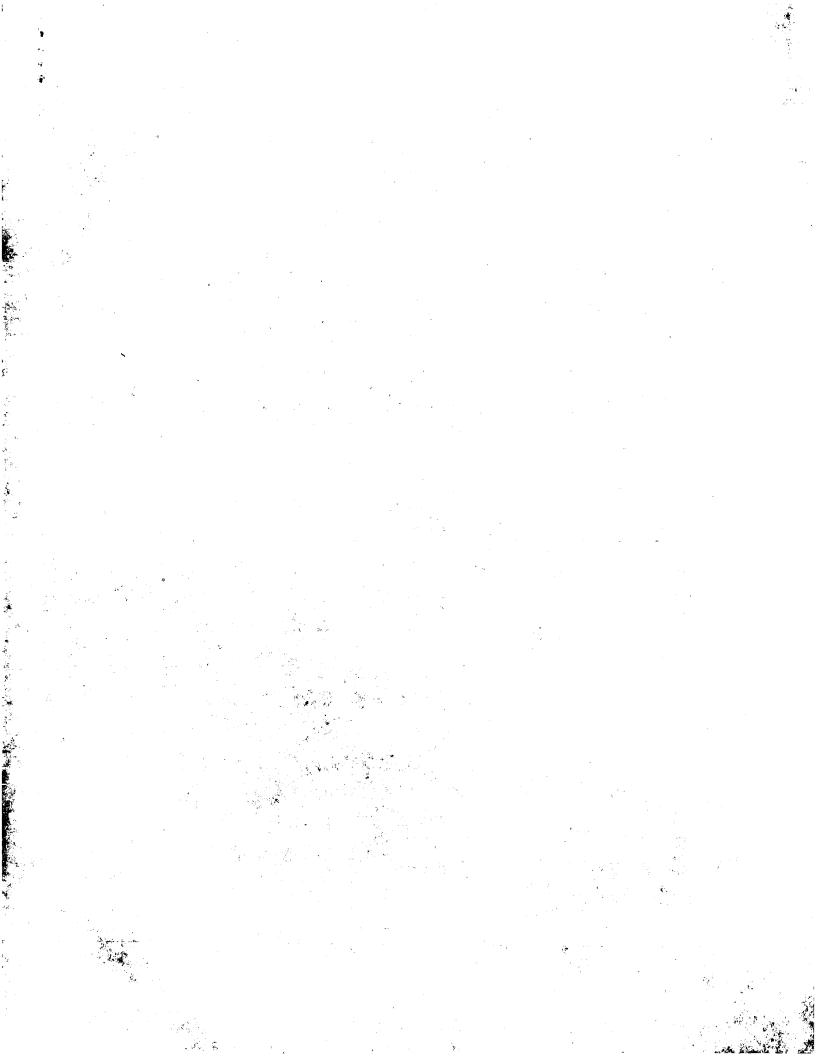
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ProDom; P
PROSITE;
                                                                                             Kirma N., Ferreira J.L., Baumstark B.R.;
"Characterization of six type A strains of Clostridium b contain type B toxin gene sequences.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF295926; AAK97132.1;
SEQUENCE 1291 AA; 150824 MW; D7CA07BAE2EB8CD2 CRC64;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurotoxin;
SEQUENCE
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                                                                                                                                                               STRAIN-1436;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=1491;
                                                                                                                                                                                                          Clostridium.
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PD001963; BONTOXILYSIN.
PD001963; BONTOXILYSIN; 1.
; PS00142; ZINC_PROTEASE; UNKNOWN_1.
xin; Transmembrane; Hydrolase; Metalloprotease; Z:
xin; Transmembrane; Hydrolase; Metalloprotease; Z:
E 1291 AA; 150513 MW; 71BCAFE23D69FAAA CRC64;
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Q46027
Q93LJ8
Q93LJ6
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Q9JXT3
Q9HXW8
Q9WR17
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Q9JEA9
Q9JEA9
062398
1 Q91YD5
219736
2 Q10734
2 Q9QTG7
Q9LBS7
Q9LBS7
Q45849
Q9ZAJ8
Q08077
Q93G71
                                                           Q9FVZ5
Q9X708
Q9EMU0
6 Q9TE21
Q9U211
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Q9YYS3
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Q9hxw8 pseudomonas
Q9wr17 african cas
Q9jea9 cassava gem
Q9jea2 cassava gem
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Q9504 archaeoglob
Q9fvz5 cryya sativ
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Q46027 clostridium
Q931j8 neisseria m
Q931j6 neisseria l
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__SEQUENCE_OF 635-1000 FROM N.A.
STRALN=NCTC 1028;
STRALNE-NCTC 1028;
MEDILINE-94013372; PubMed=8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
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057236, Q45863;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BOTULINUM NEUROTOXIN TYPE F (BONT/F PROTEIN).
BONT/F.
Clostridium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                         SEQUENCE OF 1-27 FROM N.A.

STRAIN-LANGELAND:

STRAIN-LANGEDAND:

STRAIN-LANGEDAND:

MEDI-ARTS-96040102; PubMed-9732534;

East A.K., Bhandari M., Hielm S., Collins M.D.;

"Analysis of the botulinum neurotoxin type F gene clusters in proteolytic and nonproteolytic Clostridium botulinum and Clostridium barati.";
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STRAIN-NCTC 10281;
Hutson R.A., Collins M.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
Curr. Microbiol. 37:262-268(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SIDNIER M.J., Bodsworth N.J., Wheten S.M., Minton N.F.;

Submitted (AUG_1994) to the EMBL/GenBank/DDBJ databases.
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Q9ZAJ5;
Q1-MAY-1999
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; U
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EMBL;
EMBL;
HSSP;
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InterPro; IPR000310; Zn_WTpeptdse.
Pfam; PF01742; Peptidase. W27; 1.
PRINTS; PR00760; BONTOXILYSIN.
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neurotoxins.";
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MEDLINE-98440323; PubMed-9767710;
Santos-Buelga J. Collins M.D. E
"Characterization of the genes en
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ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1280 AA; 147487 MW; D0F748976EBC222C
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£135496; AAA23210.1;

$x70821; CAA50152.1;

$x99064; CAA67512.1;

$p10845; 3BTA.
                    SISDYINKWIFVTITNURLGNSRIYINGNLI
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P10845; 3BTA.
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Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PROBOm; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNI
SEQUENCE 1268 AA; 145513 MW; 96:
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01-OCT-2000
01-OCT-2000
01-DEC-2001
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                                  SEQUENCE FROM N.A.
STRAIN-LCL 155 (KZ 1885);
Wang X., Maegawa T., Kozaki S.,
Kato H., Nakamura S., Karasawa
"C. butyricum (LCL 155) gene fo
                                                                                                                                                                                                                                                                                                                                                                                TYPE
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                                                                                                                                                                    Wang X., Maegawa
Karasawa T.;
"C. butyricum (LC
                                                                                                                                                                                                                                                                                 Clostridium.
NCBI_TaxID=1492;
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Clostridium
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Submitted (JAN-2000) [3]
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MEDLINE-93252228;
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                   EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ databases.
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                                      for type E botulinum toxin.";
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Pred. No.
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Karasawa T.;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Karasawa T.;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Karasawa T.;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Karasawa T.;
"C. butyricum (KZ 1887) qene for type E botulinum toxin ":
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Karasawa T.;
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STRAIN-KZ 1886;
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Submitted (JAN-2000) to
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Karasawa T.;
"C. butyricum (KZ 1898) gene for type E botulinum toxin "·
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Karasawa T.;
"C. butyricum (KZ 1899) gene for type E botulinum toxin.";
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butyricum (KZ 1891) gene for type E botulinum toxin."; nitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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RE STRAIN-BL 6340/ATCC 43755/BL 5520/KZ 147;

RX MEDLINE-20509829; PubMed=11055954;

RX MEDLINE-20509829; PubMed=11055954;

RA WANG X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,

RA Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;

RT Menertc Analysis of Type E Botulinum Toxin-Producing Clostridium

RT butyricum Strains.";

RL Appl. Environ. Microbiol. 66:4992-4997(2000).

DR REMBL; AB039264; BAB12249.1; -.

DR HISSP; P10845; 3BTA.

DR HISSP; P10845; 3BTA.

DR HISSP; P10845; 3BTA.

DR HITCPPTO; IPR000139; Bontoxilysin.

DR Fifam; PF01742; Peptidase. M27; 1.

DR PFAm; PF00760; BONTOXILYSIN.

DR PRINTS; PR00760; BONTOXILYSIN.

DR PROSITE; P800142; ZINC_PROTEASE; UNKNOWN_1.

DR PROSITE; P500142; ZINC_PROTEASE; UNKNOWN_1.
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Q9FAR6;
01-MAR-2001
01-MAR-2001
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                                                                                                    Q45894 PRELIMINARY; PRT; 1296 AA. Q45894; P77780; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat BGTULLINUM NEUROTOXIN TYPE A (TYPE A NEUROTOXIN).
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF001742; Reptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOD; PD001963; BONTOXILYSIN, 1.
PROSSTTE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
PROSSTTE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1251 AA; 143751 MW; 2021F4E427070296 CRC64;
    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                           Clostridium botulinum
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01-JUN-2001
01-JUN-2001
01-DEC-2001
            SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDIXWE-21173698; PubMed-11259647;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
                                                                                                                                                                                                                                                                                        Caulobacter crescentus.
Bacteria; Proteobacteria;
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East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
gene encoding the nontoxic nonhemagglutinin component.";
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                                                                                                                                                                                                                                                                    Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             components of Clostridium botulinum type A progenitor toxins FEBS Lett. 376:41-44(1995).
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Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujita R., Fujinaga Y., Inoue K., N
"Molecular characterization of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96096783; PubMed=8521962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-TYPE A NIH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-18 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=62A;
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C; X92973; CAA63551.1; -. 

C; X87974; CAA61234.1; -. 

C; D67030; BAA11051.1; -. 

P) P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIFVTITNNRL
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                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                      subdivision;
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Tepuc..., Gwinn M.L., na...
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RESULT
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Best Local S
Matches
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01-DEC-2001
01-DEC-2001
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Q62080;
SEQUENCE FROM N.A.

MEDLINE=92331628; PubMed=1628631;
Oltz E.M., Yancopoulos G.D., Morrow M.A.,
Kaplan K., Gillis S., Melchers F., Alt F.V
"A novel regulatory myosin light chain ger
subsets and is IL-7 inducible.";
EMBO J. 11:2759-2767(1992).
                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
SEQUENCE
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HSSP; P13543; ISCM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BUA6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EMBL; AE005758; AAK22798.1; -. TIGR; CC0813; -.
                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                MYLC2PL.
                                                                                                                                                                                                                                               MYOSIN LIGHT
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8; Conservative
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131 AA;
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1PR002048; EF-hand; UNKNOWN_1.
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| (Tremblrel. 19, I
| (Tremblrel. 19, I
| (Tremblrel. 19, I
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                                                                                                                                                                      Chordata;
Rodentia;
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                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
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Catarrhini;
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72BC45442BEF99FD CRC64;
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PRECURSOR LYMPHOCYTE-SPECIFIC.
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28;
                                      F.W.;
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                                                                             Lee
                                                                                                                                                                        Murinae;
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RESULT 10
095023
ID 095023
AC 095023
DT 01-MAY
DT 01-MAY
DT 01-MAY
DT 01-MEC
CE WUGSC:
OE WUGSC:
OE WARMA
OX WCBI.
RN [1]
RP [2]
RESULT 11

Q85641

ID Q85641

AC Q85641

AC Q85641

D7 01-NOV

D7 01-NOV

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D6 3' ENV GE

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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-I-SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
EMBL; AC004953; AAD08850.1;
-EMBL; BENDL;                                                                                                                                                                                                                                                                                                                                                                          Q85641
Q85641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Geisel C., Kalicki J., Gibson A.;

"The sequence of Homo sapiens PAC clone RP5-1059M17.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                01-NOV-1996 (TrembLrel. 01, Created)
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-JUN-2001 (TrembLrel. 17, Last annotation update)
3' END OF THE GENOME OF MOLONEY MURINE LEUKEMIA VIRUS (CODES FOR THE ENV GENE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
WUGSC:H_DJ1059M17.2 PROTEIN (FRAGMENT).
WUGSC:H_DJ1059M17.2.
SEQUENCE FROM N.A.
                                                                                                     Moloney murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1891705; Mylc2p1.
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                                                                  NCBI_TaxID=11801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 FKVFDTE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 FKVFDTE 80
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T; SM00054; EFh; 2.
TTE; PS00018; EF_HAND; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.9%; So lilarity 100.0%; I Conservative 0;
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100.0%; Prr
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            182 AA.
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o. 33;
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RESULT
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RR RP OC S
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Q83401
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Best Local Similarity
Matches 7; Conserv
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Best Local
                                                            O83401 PRELIMINARY; PRT; 187 AA.

(083401;
(01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POLYPROTEIN PRECURSOR (FRAGMENT).

Moloney murine sarcoma virus.

Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.

NCBL_TaxID-11809;
[1]
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085640;
085640;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MOLONEY MURINE LEDEMENT AURUS (M-MULV) TRANSPOSON GENES AND
REPLICATING DETAILS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81013872; PubMed-6251454;
Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
"Nucleotide sequence of Moloney leukemia virus: 3' end reveals details
of replications, analogy to bacterial transposons, and an unexpected
gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-81052384; PubMed-6159543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutcliffe J.G., Shinnick T.M., Lerner R.A.;

"Moloney murine leukemia virus is a transposon: Nucleotide sequence analysis identifies genes and replication details.";

Cold Spring Harb. Symp. Quant. Biol. 45:707-710(1981).

EMBL; M12997; AAA46529.1;

EMBL; M12997; AAA46529.1;

HSSP; P03385; IMOF.

IRSOP; P03085; IMOF.

IRSOP; P030850; ERV_P01yprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus
NCHI_TaxID=11786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00429; ENV_polyprotein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 EKSISNL 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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100.0%; Pred. No. 38
tive 0; Mismatches
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o. 38;
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Best Local S
Matches 7
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Best Local 9
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01-CCT-2000 (TrembLrel. 15, C:
01-CCT-2000 (TrembLrel. 15, L:
01-DEC-2001 (TrembLrel. 19, L:
PUTATIVE MEMBRANE PROTEIN.
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:655-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene."
Proc.
EMBL;
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Campylobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 6-187 FROM N.A.
MEDLINE-81013872; PubMed-6251454;
Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner J
"Nucleotide sequence of Moloney leukemia virus: 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;

Terner R.A.;

The sequence allows detection of a new retroviral gene product.";
                                                                                                                                          Complete proteome. SEQUENCE 200 AA;
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                            Campylobacter jejuni.
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         15
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| EKSISNL 48
                                                       KTEIETL 89
                                          KTEIETL
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                                                                                                                                                                AL139078; CAB73906.1; -.
                                                                                    l Similarity
7; Conserv
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95
187
                                                                                     Conservative
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                                           72
                                                                                                                                           AA;
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187 F
20841 MW;
                                                                               4.9%; 5c.
100.0%; Pr
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                                                                                                                                           22387 MW;
                                                                                                                                                                                                                                                                                                                                epsilon subdivision; Campylobacter group;
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Last annotation update)
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POTENTIAL.
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-:- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING EMBL; X65981; CAA46796.1; -.

HSSP; P13543; ISCM.

MGD; MGI:1891705; Mylc2pl.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 2.

PROSITE; PS00018; EF_HAND; UNKNOWN_1.
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Q1-NOV-1996
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EMBO J. 11:2759-2767(1992).
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SEQUENCE 202 AA;
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Mammalia; Eutheria; Rodentia;
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HSSP; P10845; 3BTA.
MEROPS; M27.002;
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InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000139; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01742; Peptidase_A7; 1.
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ProDom; PD001963; Bontoxilysin; 1.
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MEDLINE-98440323; PubMed-976710;
Santos-Buelga J., Collins M.D., E
"Characterization of the genes en
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RESULT
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Best Local S
Matches 16
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF001742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOm; PF001963; BONTOXILYSIN; 1.
PROSITE; PS001142; ZINC_PROTEASE; UNK
SEQUENCE 1268 AA; 145513 MW; 963
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01-JUN-2001
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01-NOV-1996
01-DEC-2001
STRAIN-97ZA012;
Rodenburg C.M., Li Y., Trask S./Allen S., Shaw G.M., Hahn B.H.,
Submitted (JUL-2000) to the EMBH
EMBL; AF286227; AAK30993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q994N3;
Q994N3;
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                                                                                                                                                      MEDLINE-21094715; PubMed-11177395;
Rodenburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robert Kallsh M.L., Shaw G.M., Allen S., Hahn B.H., Gao F.;
Kallsh M.L., Shaw G.M., Allen S., Hahn B.H., Gao F.;
"Near full-length clones and reference sequences for subtype isolates for HIV type I from three different continents.";
AIDS Res. Hum. Retroviruses 17:161-168(2001).
                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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Bacteria; Firmicutes;
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             STRAIN-97ZA012;
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MEDLINE-93252228;
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tson R.A., East
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                                                                  Trask S.A., Chen Y.,
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Last sequence up
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963040091AC15ED2 CRC64;
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                                                                    Decker J.,
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RESULT
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Q9BPLO;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FTZ-F1.
FTZ-F1.
Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Schistosomatoidea; Schistoso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subtype C accessory genes.";
AIDS Res. Hum. Retroviruses 17:775-781(2001).
EMBL; AF325755; AAK09163.1; -
InterPro; IPRO00012; HIV_OREXR.
Pfam; PF00522; VPR; 1
PRINTS; PR00444; HIVVPRVPX.
SEQUENCE 96 AA; 11450 MW; 663D5ED56DED0447 CRC64;
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01-JUN-2001
01-DEC-2001
SEQUENCE FROM N.A.

Mendonca R.I., Bouton D., Vanacker J.-M., Laudet V., Pierc Mendonca R.I., Bouton D., Vanacker J.-M., Laudet V., Pierc Mendonca and functional characterization of a Schistosoma homologue of the FTZ-F1 nuclear receptor.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCILIUIAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99BN5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-21322026; PubMed-11429118;
Scriba T.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
van Rensburg E.J.;
van Rensburg E.J.;
"Characterization and phylogenetic analysis of South African HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q9X395,
Q1-OCT-2000 (TIEMBLIFE1 15, C
Q1-OCT-2000 (TIEMBLIFE1 15, I
Q1-DEC-2000 (TIEMBLIFE1 19, I
TYPE E BOTULINUM TOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIMTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
SMARF; SM00430; HOLI; 1.
SMARF; SM00399; ZDF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
PROSITE; PS00031; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-c4.
    Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura Karasawa T.;
"C. butyricum (KZ 1898) gene for type F bofulinum fovin ".
                                                              STRAIN-KZ 1898;
                                                                                   SEQUENCE FROM N.A.
                                                                                                                       "C. butyricum (KZ 1897) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
                                                                                                                                                                                                           STRAIN-KZ 1897
                                                                                                                                                                                                                                                                                                                                   Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-KZ 1899;
                                                                                                                                                                                                                                                                                                                                                                                                                "C. butyricum (LCL 155) gene for type E botulinum toxin."; submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang X., Maegawa T., Kozaki S., Tsukamoto K., Gyobu Y., Yamakawa
Kato H., Nakamura S., Karasawa T.;
"C. butyricum (LCL 155) gene for type E botulinum toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-LCL 155 (KZ 1885);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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HSSP; P03372; 1HCQ.
                                                                                                                                                                Karasawa T
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Submitted (JAN-2000) to
                                                                                                                                                                                                                                                                                                             Karasawa T.;
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butyricum (KZ 1898) gene
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NCE 731 AA; 78130 MW; 20129AF9AAF30175 CRC64;
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8; Conserv
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100.0%; Prr
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  type E botulinum toxin.";
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNK
SEQUENCE 1251 AA; 143751 MW; 202
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MEROPS; M27.002;
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Mismatches
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Clostridium.
                                                  Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell
Remmel B., Rose M., Schlueter T., Sinoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria innocua.

Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID=1642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium butyricum Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                             PubMed-11679669;
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STRAIN-CLIP 11262
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Interpro; IPR000395; Bontoxilysin.
Interpro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
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EMBL; AB039264; BAB12249.1;
HSSP; P10845; 3BTA.
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PRODOM; PD001963; BONTOXILYSIN
PROSTITE; PS00142; ZINC_PROTEAS;
SEQUENCE 1255 AA; 143918 MW
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ZINC_PROTEASE;
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Complete proteome.
SEQUENCE 67 AA: 787% ...
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Submittedd (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000338; AAB70135.1;
EMBL; AF000334; AAB70131.1;
EMBL; AF000336; AAB70133.1;
EMBL; AF000336; AAB7013.1;
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MEDLINE-9835232; PubMed-9658150;
MEDLINE-9835232; PubMed-9658150;
Meditine-nance of an intect human immunodeficiency virus following mother-to-infant transmission.";
J. Virol. 72:6937-6943(1998).
EMBL; AR642966; ARC41130.1; -.
InterPro; IPR000012; HIV_ORFXR.
Pfam; PF00522; VPR; 1.
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100.08; Pr.
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Pred. No.
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Pred. No.
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lo. 17;
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RESULT 12
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Best Local Similarity
Sches 7; Conserv
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089654;
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01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98325222; PubMed-9658150;
Yedavalli V.R., Chappey C., Almad N.;
"Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
J. Virol, 72:6937-693(1998).
EMBL; AF042967; AAC41131.1;
Interpro; IPR000012; HIV_ORFXR.
Pfam; PF00522; VPR; 1.
PFANTS; PR0444; HIVUPRVPX.
NON_TER
96
96 AA; 11320 MW; 5995598CDF0E7FBD CRC64;
                                                              SEQUENCE FROM N.A.
STRAIN-INFANT PAIR D;
MEDLINE-98325222; PubMed-9658150;
Yedavalli V.R., Chappey C., Ahmad N.;
"Maintenance of an intact human immunodeficiency virus type 1 vpr gene
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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            following mother-to-infant transmission. J. Virol. 72:6937-6943(1998). EMBL; AF042983; AAC41147.1; -.
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STRAIN-MOTHER PAIR D;
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InterPro; IPR000012; HIV_ORFXR
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56 GVEVIIR 62
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Conservative
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(TrEMBLrel. 19, Last annotation updat
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Pred. No.
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01-NOV-1998
01-DEC-2001
VPR PROTEIN
SEQUENCE FROM N.A.
STRAIN-INFANT PAIR D;
STRAIN-INFANT PAIR D;
MEDLINE-9835822; PubMed-9658150;
MEDLINE-9835822; PubMed-9658150;

"Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
J. Virol. 72:6937-6943(1998).
EMBL; AF042991; AAC41155.1; -.
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PRINTS; PR00444; HIVVPRVPX.
NON_TER 96 96
SEQUENCE 96 AA; 11329 MW
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STRAIN-INFANT PAIR D;
MEDLINE-9832522; PubMed-9658150;
MEDLINE-9832522; PubMed-9658150;
Yedavalli V.R. (Chappey C., Ahmad N.;
"Maintenance of an intact human immunodeficiency virus type 1
"Maintenance of an intact human immunodeficiency virus type 1
following mother-to-infant transmission.";
J. Virol. 72:6937-6943(1998).
EMBL; AF04299; AAC41154.1; -.
InterPro; IPR000012; HIV_ORFXR.
Pfam; PF00522; VPR; 1.
                                                                                                                                                                                 Viruses; Retroid
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae;
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NON_TER 96 96
SEQUENCE 96 AA; 11320 MW
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56 GVEVIIR
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Pred. No.
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Pred. No.
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057236 clostridium
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09x708 clostridium
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    Curr. Microbiol. 37:262-268(1998).
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534; S., Collins M.D.; urotoxin type F gene cluc Clostridium botulinum	Z; M.D.; of the botulinal neur toxin types B, E, and 2(1993).	8542; lins M.D.; lon of the botulinal neur eurotoxin types B, E, and 2262(1993).	Clostridium group; L/GenBank/DDBJ data ALIGNMENTS PRT; 1278 AA. Created) Last sequence update) Last annotation update) (BONT/F PROTEIN).	ALIGNMENTS	092AJB 093G71 093G71 093JK0 093G71 093JK0 099G53 042077 049G53 042077 089G79 089G79 089G79 089G79 089G79 089G79 089G79 089G79 089G79 089G79 089G79 089G79 089G79 090D29 09	
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MEROPS; M27.002; ...

InterPro; IPR000395; Bontoxilysin.

InterPro; IPR00030; Zn_mTpeptdse.

Pfam; PF01742; Peptidase_M27; 1.

PRINTS; PR00760; BONTOXILYSIN; 1.

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PROSTIE; PS00142; ZNC_PROTEASE; UNK
PROSTIE; PS001442; ZNC_PROTEASE; UNK
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SEQUENCE
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MEDLINE-93252228; PubMed-8486245;
MEDLINE-93252228; PubMed-8486245;
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SEQUENCE 1280 AA; 147487 MW; D
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Pfam; PF01742; Peptidase_M27; 1.
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Curr. Microbiol. 37:312-3
EMBL; Y13631; CAA73972.1;
HSSP; P10845; 3BTA.
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Wang X., Maegawa T.,
Karasawa T.;
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"C. butyricum (LCL 155) gene for type E botulinum toxin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                   SEQUENCE FROM N.A.
STRAIN-KZ 1890;
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Karasawa T.;
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Karasawa T.;
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STRAIN=KZ 1899;
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                                                                                                                                                          butyricum (KZ 1889)
mitted (JAN-2000) to
                                                                                                                                                                                                                                                                                                                                                 butyricum (KZ 1886)
mitted (JAN-2000) to
                                                                              butyricum (KZ 1890)
                                                                                                     X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
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to the EMBL/GenBank/DDBJ databases.
            Kozaki S.,
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the EMBL/GenBank/DDBJ databases.
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the EMBL/GenBank/DDBJ databases.
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the EMBL/GenBank/DDBJ databases.
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the EMBL/GenBank/DDBJ databases.
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            Tsukamoto
            ×.
            Kato H.,
             Nakamura
            s.
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Best Local
InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; Pf01742; Peptidase_MZ7; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; BONTOXILYSIN; 1.
PROSTIE; PS00142; ZINC_PROTEASE; UNK
SEQUENCE 1255 AA; 143918 MW; 1B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9FAR6, PRELIMINARY; PRT; 1255 AA.

O9FAR6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                              MEDLINE-20509829; PubMed-11055954;
Wang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
"Genetic Analysis of Type E Botulinum Toxin-Producing Clostridium
butyricum Strains.";
Appl. Environ. Microbiol. 66:4992-4997(2000).
EMBL, AB039264; BAB12249.1;
HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BL 6340/ATCC 43755/BL 5520/KZ 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium butyricum. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BONT/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE E BOTULINUM TOXIN
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Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS001042; ZINC_PROTEASE; UNKNOWN_1.
PROSITE; PS001042; ZINC_PROTEASE; UNKNOWN_1.
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submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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p; P10845; 3BTA.
PS; M27.002; -
pppo: TT-
p; P1087.002; -
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the EMBL/GenBank/DDBJ databases.
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Pred. No. 8.4e-06;
0; Mismatches 0;
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     UNKNOWN_1.
1B557B9D85CD8E4D CRC64;
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01.NOV-1996 (TremBLrel. 01,
01-NOV-1996 (TremBLrel. 01,
01-OCT-2000 (TremBLrel. 15,
BOTULINUM NEUROTOXIN TYPE E
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NON_TER
SEQUENCE
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01-NOV-1996 (TremBLrel. 01,
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01-OCT-2000 (TremBLrel. 15,
BOTULINUM NEUROTOXIN TYPE E
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MEDLINE-94013372; PubMed-8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                         STRAIN-TYPE E, VH (DOLMAN);
MEDLINE=94013372; PubMed=8408542;
Campbell K., East A.K., Collins M
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NON_TER
                                                                                                           specific identifica
J. Clin. Microbiol.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Clostridium.
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                                                                                    probes for identification of the botulinal neurotoxin fic identification of neurotoxin types B, E, and F."; in. Microbiol. 31:2255-2262(1993).
X70818; CAA50149.1; -.
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(FRAGMENT).
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Pred. No.
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EMBL; X73423; CAA51824.1; -.

EMBL; X92973; CAA63551.1; -.

EMBL; X92973; CAA61234.1; -.

EMBL; D67030; BAA11051.1; -.

HSSP; P10845; BFFA.
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Q45894; P77780;
01-NOV-1996 (TremBLrel. 01, C
01-NOV-1996 (TremBLrel. 01, L
01-DEC-2001 (TremBLrel. 19, L
BOTULINUM NEUROTOXIN TYPE A (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Willems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridiu
botulinum type A associated with infant botulism: comparison
other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97016817; PubMed=8863443;
East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
1014 WIFVTITNNRL 1024
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Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
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MEDLINE-96096783; PubMed-8521962;
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e neurotoxin of Clostridium
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                                                                                                                                                                                        Scriba T.J., Treurnicht F.K., Zeier M., Engelbrecht S., van Rensburg E.J.; van Rensburg E.J.; "Characterization and phylogenetic analysis of South African HIV-1 subtype C accessory genes."; ALDS Res. Hum. Retroviruses 17:775-781(2001).
EMBL; AF325755; AAK09162.1; ...
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Rodenburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robertson Ralish M.L., Shaw G.M., Allen S., Hahn B.H., Gao F.;
"Near full-length clones and reference sequences for subtype C isolates for HIV type 1 from three different continents.";
AIDS Res. Hum. Retroviruses 17:161-168(2001).
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                                                                            PRINTS; PRO0444; HIVVPRVPX.
PRINTS; PRO0444; HIVVPRVPX.
PROUENCE 96 AA; 11450 MW;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF286227; AAK30993.1; -
InterPro; IPR000012; HIV_ORFXR.
Pfam; PF00522; VPR; 1.
PRINTS; PR00522; VPR; 1.
PRINTS; PR005444; HIVVPRVPX.
SEQUENCE 96 AA; 11415 MW; 839CB1B0999C059B CRC64;
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STRAIN-97ZA012;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                     InterPro; IPR000012; HIV_ORFXR. Pfam; PF00522; VPR; 1.
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Viruses, Retroid viruses; Retroviridae; Lentivirus
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                                                     STRAIN-TYPE B, NON-PROTECLYTIC EKLUND 2B (COLWORTH 229);
MEDLINE-94013372; PubMed-8406547;
Campbell K, East A, K, Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and "gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
EMBL; X70819; CAA50150:1; --
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MEDLINE-94013372; PubMed-8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene
specific identification of neurotoxin types B, E, and F.";
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                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=1491;
                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                 Clostridium botulinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium.
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                                             ISSP;
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P10845; 3BTA.
                                            P10845; 3BTA.
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42131 MW;
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42175 MW;
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 A2E0FFFC81F9533D CRC64;
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Q9A9Z8;
Q1-JUN-2001
01-JUN-2001
01-DEC-2001
SEQUENCE ENUM N.A.

STRAIN=ATCC 19089 / CB15;

MEDLINE=21173698; PubMed=11259647;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K. Risen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh
                                                                                                                                                                                                                                                                                                                                                                                                             binding domains. J. Cell Sci. 112: EMBL; AJ242628; (
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Q9X708;
Q1-NOV-1999 (TrEMBLrel. 12,
Q1-NOV-1999 (TrEMBLrel. 12,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                      Caulobacter crescentus.
Bacteria; Proteobacteria;
                                                                                                                                                                    HYPOTHETICAL
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Clostridium botulinum.
                                                                                                                               Caulobacter
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                                                                                                SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=69394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schiavo
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llarity 100.0%;
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SMART; SM0039; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
DNA-binding; Nuclear protein; Receptor; Transczinc-finger.
SEQUENCE 731 AA; 78130 MW; 20129AF9AAF3017
                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL; AE005758; AAK22798.1; -.
TIGR; CC0813; -.
Hypothetical protein; Complete proteome.
SEQUENCE 540 AA; 59648 MW; 72BC45442BEF99FD CRC64;
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Schistosomatoidea; S
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01-DEC-2001
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                                                                                                                                                                                                                                           NCBI_TaxID=6183;
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Schistosomatidae;
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32;
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